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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Apr 08	"Ask CAS" for self-help around the clock
NEWS 3	Apr 09	BEILSTEIN: Reload and Implementation of a New Subject Area
NEWS 4	Apr 09	ZDB will be removed from STN
NEWS 5	Apr 19	US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
NEWS 6	Apr 22	Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
NEWS 7	Apr 22	BIOSIS Gene Names now available in TOXCENTER
NEWS 8	Apr 22	Federal Research in Progress (FEDRIP) now available
NEWS 9	Jun 03	New e-mail delivery for search results now available
NEWS 10	Jun 10	MEDLINE Reload
NEWS 11	Jun 10	PCTFULL has been reloaded
NEWS 12	Jul 02	FOREGE no longer contains STANDARDS file segment
NEWS 13	Jul 22	USAN to be reloaded July 28, 2002; saved answer sets no longer valid
NEWS 14	Jul 29	Enhanced polymer searching in REGISTRY
NEWS 15	Jul 30	NETFIRST to be removed from STN
NEWS 16	Aug 08	CANCERLIT reload
NEWS 17	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 18	Aug 08	NTIS has been reloaded and enhanced
NEWS 19	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS 20	Aug 19	IFIPAT, IFICDB, and IFIUDB have been reloaded
NEWS 21	Aug 19	The MEDLINE file segment of TOXCENTER has been reloaded
NEWS 22	Aug 26	Sequence searching in REGISTRY enhanced
NEWS 23	Sep 03	JAPIO has been reloaded and enhanced
NEWS 24	Sep 16	Experimental properties added to the REGISTRY file
NEWS 25	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 26	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 27	Oct 21	EVENTLINE has been reloaded
NEWS 28	Oct 24	BEILSTEIN adds new search fields
NEWS 29	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 30	Oct 25	MEDLINE SDI run of October 8, 2002
NEWS 31	Nov 18	DKILIT has been renamed APOLLIT
NEWS 32	Nov 25	More calculated properties added to REGISTRY
NEWS 33	Dec 02	TIBKAT will be removed from STN
NEWS 34	Dec 04	CSA files on STN
NEWS 35	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 36	Dec 17	TOXCENTER enhanced with additional content
NEWS 37	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS 38	Dec 30	ISMEC no longer available
NEWS 39	Jan 13	Indexing added to some pre-1967 records in CA/CAPLUS
NEWS 40	Jan 21	NUTRACEUT offering one free connect hour in February 2003
NEWS 41	Jan 21	PHARMAML offering one free connect hour in February 2003
NEWS 42	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS 43	Feb 13	CANCERLIT is no longer being updated
NEWS 44	Feb 24	METADEX enhancements
NEWS 45	Feb 24	PCTGEN now available on STN

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 NEWS 46  Feb 24  TEMA now available on STN
 NEWS 47  Feb 26  NTIS now allows simultaneous left and right truncation
 NEWS 48  Feb 26  PCTFULL now contains images
 NEWS 49  Mar 04  SDI PACKAGE for monthly delivery of multifile SDI results

 NEWS EXPRESS  January 6 CURRENT WINDOWS VERSION IS V6.01a,
               CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 17:46:35 ON 12 MAR 2003

=> file medline, uspatful, dgene, wpids, embase
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                 1.05       1.05

FILE 'MEDLINE' ENTERED AT 17:49:36 ON 12 MAR 2003

FILE 'USPATFULL' ENTERED AT 17:49:36 ON 12 MAR 2003
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FILE 'DGENE' ENTERED AT 17:49:36 ON 12 MAR 2003
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FILE 'WPIDS' ENTERED AT 17:49:36 ON 12 MAR 2003
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FILE 'EMBASE' ENTERED AT 17:49:36 ON 12 MAR 2003
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=> s exogenous DNA or gene
   3 FILES SEARCHED...
L1     3220110 EXOGENOUS DNA OR GENE

=> s l1 and integrate into yeast chromosome
L2            0 L1 AND INTEGRATE INTO YEAST CHROMOSOME

=> s l1 and yeast chromosome
L3         1032 L1 AND YEAST CHROMOSOME

=> s l3 and integrate yeast chromosome
L4            1 L3 AND INTEGRATE YEAST CHROMOSOME

=> d l4 ti abs ibib tot
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L4 ANSWER 1 OF 1 WPIDS (C) 2003 THOMSON DERWENT
TI Yeast derived vector contg. **gene** for antibiotic resistance - controlled by yeast or synthetic promoter, able to integrate with **yeast chromosome**.
AN 1985-304934 [49] WPIDS
CR 1986-332093 [50]; 1996-189959 [20]
AB EP 163491 A UPAB: 19960529
Vector includes a **gene** for resistance to an antibiotic normally able to kill a host yeast cell, and the **gene** is transcribed from a yeast or synthetic promotor sequence. The vector can be integrated into a chromosome of the yeast host.

The vector may also contain (1) a **gene** heterologous to the host and (2) a homologous sequence of the chromosome, inserted in such a way that no interference with host metabolism occurs.

USE/ADVANTAGE - Yeast cells transformed with the vectors express e.g. glucoamylase (able to convert starch to glucose which is the converted to CO2 or EtOH, for use in dough making or brewing). Those expressing malate permease are useful in wine making because they can eliminate malic acid. The heterologous **gene** can also express a therapeutically useful protein, e.g. interferon. These vectors are stable over many generations even in the absence of selection.

Dwg.0/4

Dwg.0/4

ABEQ EP 163491 B UPAB: 19960428
A yeast cell transformed by integration into a chromosome thereof of vector DNA; characterised in that the host yeast cell is an industrial non-haploid yeast cell; in that the vector DNA comprises a **gene** for resistance to an antibiotic otherwise capable of killing said yeast cell, said **gene** being transcribed from a promoter sequence which is capable of promoting the expression of said antibiotic resistance **gene** at a level which confers antibiotic resistance to said cell; in that said vector DNA comprises a sequence homologous with a sequence of said chromosome and is integrated therein; and in that said vector DNA further comprises a **gene** for a desired heterologous protein.

Dwg.0/4

ACCESSION NUMBER: 1985-304934 [49] WPIDS
CROSS REFERENCE: 1986-332093 [50]; 1996-189959 [20]
DOC. NO. CPI: C1985-131759
TITLE: Yeast derived vector contg. **gene** for antibiotic resistance - controlled by yeast or synthetic promoter, able to integrate with **yeast chromosome**
.
DERWENT CLASS: B04 D16
INVENTOR(S): YOCUM, R R
PATENT ASSIGNEE(S): (YOCU-I) YOCUM R R; (OMNI-N) OMNIGENE INC; (BIOY) BIOTECHNICA INT INC
COUNTRY COUNT: 7
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 163491	A	19851204	(198549)*	EN	27
AU 8542709	A	19851128	(198604)		
BR 8502400	A	19860121	(198610)		
FI 8502024	A	19851123	(198611)		
JP 61040793	A	19860227	(198615)		
DK 8502241	A	19851123	(198617)		
EP 163491	B1	19960327	(199617)	EN	20
DE 3588096	G	19960502	(199623)		
CA 1338857	C	19970121	(199715)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE

EP 163491	B1	EP 1985-303625	19850522
DE 3588096	G	DE 1985-3588096	19850522
		EP 1985-303625	19850522
CA 1338857	C	CA 1985-481908	19850521

FILING DETAILS:

PATENT NO	KIND		PATENT NO
DE 3588096	G	Based on	EP 163491

PRIORITY APPLN. INFO: US 1984-612796 19840522

=> d his

(FILE 'HOME' ENTERED AT 17:46:35 ON 12 MAR 2003)

FILE 'MEDLINE, USPATFULL, DGENE, WPIDS, EMBASE' ENTERED AT 17:49:36 ON 12 MAR 2003

L1 3220110 S EXOGENOUS DNA OR GENE
L2 0 S L1 AND INTEGRATE INTO YEAST CHROMOSOME
L3 1032 S L1 AND YEAST CHROMOSOME
L4 1 S L3 AND INTEGRATE YEAST CHROMOSOME

=> s l3 and integrative transformation
L5 29 L3 AND INTEGRATIVE TRANSFORMATION

=> d l5 ti abs ibib tot

L5 ANSWER 1 OF 29 MEDLINE

TI Isolation and characterization of the RNA2+, RNA4+, and RNA11+ genes of Saccharomyces cerevisiae.

AB We used genetic complementation to isolate DNA fragments that encode the Saccharomyces cerevisiae genes RNA2+, RNA4+, and RNA11+ and to localize the genes on the cloned DNA fragments. RNA blot-hybridization analyses coupled with genetic analyses indicated the RNA2+ is coded by a 3.0-kilobase (kb) transcript, RNA4+ is coded by a 1.6-kb transcript, and RNA11+ is coded by a 1.3-kb or a 1.7-kb transcript or both; none of the cloned genes contains detectable introns. All three genes were transcribed into messages of very low abundance (approximately 20 times lower than a ribosomal protein message). DNA blot-hybridization revealed that all cloned genes are represented only once in the **yeast chromosome**. mRNA for RNA2+ and RNA4+ is produced in approximate proportion to **gene** dosage, whereas RNA11+ transcription appears to be not nearly so dependent on **gene** dosage. On a medium-copy plasmid (5 to 10 copies per cell), each cloned **gene** complemented mutations only in its own **gene**, indicating that each **gene** encodes a unique function. Genetic analysis by **integrative transformation** indicated that we cloned the RNA2+, RNA4+, and RNA11+ structural genes and not second-site suppressors.

ACCESSION NUMBER: 85054623 MEDLINE
DOCUMENT NUMBER: 85054623 PubMed ID: 6094499
TITLE: Isolation and characterization of the RNA2+, RNA4+, and RNA11+ genes of Saccharomyces cerevisiae.
AUTHOR: Soltyk A; Tropak M; Friesen J D
SOURCE: JOURNAL OF BACTERIOLOGY, (1984 Dec) 160 (3) 1093-100. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198501

ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19900320
Entered Medline: 19850118

L5 ANSWER 2 OF 29 USPATFULL
TI Genes and proteins controlling cholesterol synthesis
AB The present invention provides isolated nucleic acid sequences which encode a family of HMG-CoA Reductase Degradation (HRD) polypeptides. More particularly, the present invention provides isolated HRD1, HRD2 and HRD3 nucleic acids and the Hrd polypeptides encoded by such nucleic acids, i.e., Hrd1, Hrd2 and Hrd3, respectively. Vectors comprising the nucleic acids are provided. In addition, the present invention provides screening assay related to cholesterol biosynthesis.

ACCESSION NUMBER: 2003:67661 USPATFULL
TITLE: Genes and proteins controlling cholesterol synthesis
INVENTOR(S): Rine, Jasper D., Moraga, CA, United States
Hampton, Randolph, San Diego, CA, United States
PATENT ASSIGNEE(S): The Regents of the University of California, Oakland, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6531292	B1	20030311
APPLICATION INFO.:	US 2000-628133		20000728 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1996-699103, filed on 16 Aug 1996, now patented, Pat. No. US 6107462

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-2381P	19950817 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Saidha, Tekchand
LEGAL REPRESENTATIVE: Osman, Richard Aron
NUMBER OF CLAIMS: 9
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 10 Drawing Page(s)
LINE COUNT: 4087

L5 ANSWER 3 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I SceI and the use thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:122819 USPATFULL
TITLE: Nucleotide sequence encoding the enzyme I SceI and the use thereof
INVENTOR(S): Dujon, Bernard, Gif sur Yvette, FRANCE
Choulika, Andre, Paris, FRANCE
Perrin, Arnaud, Paris, FRANCE
Nicolas, Jean-Francois, Noisy le Roi, FRANCE
PATENT ASSIGNEE(S): Institut Pasteur, Paris, FRANCE (non-U.S. corporation)
Universite Paris VI/Universite Pierre et Marie Curie, Paris, FRANCE (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6395959	B1	20020528
APPLICATION INFO.:	US 1996-643732		19960506 (8)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1994-336241, filed

on 7 Nov 1994, now patented, Pat. No. US 5792632 Continuation-in-part of Ser. No. US 1992-971160, filed on 5 Nov 1992, now patented, Pat. No. US 5474896, issued on 12 Dec 1995 Continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Clark, Deborah J. R.
ASSISTANT EXAMINER: Paras, Jr., Peter
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 7
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 63 Drawing Figure(s); 46 Drawing Page(s)
LINE COUNT: 2587
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 4 OF 29 USPATFULL
TI Yeast genes that affect viral replication
AB An antiviral agent comprising an altered MAB1, MAB2, MAB3, or OLE1 **gene**, **gene** homologs or related genes is disclosed. In another embodiment, the present invention is a method of creating a virus resistant organism comprising creating a transgenic organism comprising an antiviral agent selected from the group of altered MAB1 genes, MAB2 genes, MAB3 genes or OLE1 genes, homologs of these genes, related genes and combinations of these genes and homologs.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:27457 USPATFULL
TITLE: Yeast genes that affect viral replication
INVENTOR(S): Ahlquist, Paul G., Madison, WI, UNITED STATES
Ishikawa, Masayuki, Sapporo, JAPAN
Diez, Juana, Barcelona, SPAIN
Price, Duane B., Mountain Brook, AL, UNITED STATES
Lee, Wai-Ming, Madison, WI, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002016305	A1	20020207
APPLICATION INFO.:	US 2001-760040	A1	20010112 (9)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1998-94069, filed on 9 Jun 1998, ABANDONED

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-49439P	19970612 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Jean C. Baker, Quarles and Brady LLP, 411 East Wisconsin Avenue, Milwaukee, WI, 53202-4497
NUMBER OF CLAIMS: 30
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 12 Drawing Page(s)
LINE COUNT: 1847
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 5 OF 29 USPATFULL
TI Genes and proteins controlling cholesterol synthesis
AB The present invention provides isolated nucleic acid sequences which encode a family of HMG-CoA Reductase Degradation (HRD) polypeptides. More particularly, the present invention provides isolated HRD1, HRD2 and HRD3 nucleic acids and the Hrd polypeptides encoded by such nucleic acids, i.e., Hrd1, Hrd2 and Hrd3, respectively. Vectors comprising the nucleic acids are provided. In addition, the present invention provides screening assay related to cholesterol biosynthesis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:235105 USPATFULL
TITLE: Genes and proteins controlling cholesterol synthesis
INVENTOR(S): Rine, Jasper D., Moraga, CA, United States
Hampton, Randolph, San Diego, CA, United States
PATENT ASSIGNEE(S): The Regents of the University of California, Oakland, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6333172	B1	20011225
APPLICATION INFO.:	US 1999-229059		19990111 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1996-699103, filed on 16 Aug 1996, now patented, Pat. No. US 6107462

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-2381P	19950817 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Nashed, Nashaat T.
LEGAL REPRESENTATIVE: Osman, Richard Aron
NUMBER OF CLAIMS: 36
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 10 Drawing Page(s)
LINE COUNT: 3308
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 6 OF 29 USPATFULL
TI Dominant selectable marker for **gene** transformation and disruption in yeasts
AB The present invention provides a novel dominant selectable marker system in yeast that is based on an aminoglycoside, nourseothricin (NST). This compound possesses a powerful antifungal activity against Candida albicans and S. cerevisiae. The invention provides a cognate drug resistance marker for use in **gene** transformation and disruption experimentation in Candida albicans and Saccharomyces cerevisiae. In particular, the invention presents: 1) direct utility for **gene** manipulations in both clinically and experimentally relevant strains regardless of genotype and without affecting growth rate, or hyphal formation; and 2) applicability to antifungal drug discovery, including target validation and various forms of drug screening assays.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:182565 USPATFULL
TITLE: Dominant selectable marker for **gene** transformation and disruption in yeasts
INVENTOR(S): Roemer, Terry, Montreal, Canada
Bussey, Howard, Westmount, Canada
Davison, John, Montreal, Canada

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2001031724	A1	20011018
APPLICATION INFO.:	US 2001-785669	A1	20010216 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-183462P	20000218 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: PENNIE AND EDMONDS, 1155 AVENUE OF THE AMERICAS, NEW

YORK, NY, 100362711
NUMBER OF CLAIMS: 24
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 1225
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 7 OF 29 USPATFULL
TI Yeast strains for the production of xylitol
AB The invention relates to novel yeast strains having a reduced ability to metabolize xylitol. The invention further relates to the use of said strains for the production of xylitol.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:125780 USPATFULL
TITLE: Yeast strains for the production of xylitol
INVENTOR(S): Apajalahti, Juha, Helsinki, Finland
Leisola, Matti, Espoo, Finland
PATENT ASSIGNEE(S): Xyrofin Oy, Espoo, Finland (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6271007	B1	20010807
APPLICATION INFO.:	US 1994-194624		19940207 (8)
RELATED APPLN. INFO.:	Continuation of Ser. No. US 1992-905870, filed on 30 Jun 1992, now abandoned		

	NUMBER	DATE
PRIORITY INFORMATION:	FI 1991-3197	19910701

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Achutamurthy, Ponnathapu
ASSISTANT EXAMINER: Rao, Manjunath N.
LEGAL REPRESENTATIVE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
NUMBER OF CLAIMS: 60
EXEMPLARY CLAIM: 1
LINE COUNT: 1096
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 8 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:78950 USPATFULL
TITLE: Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
INVENTOR(S): Dujon, Bernard, Gif sur Yvette, France
Choulika, Andre, Paris, France
Colleaux, Laurence, Edinburgh, United Kingdom
Fairhead, Cecile, Malakoff, France
Perrin, Arnaud, Paris, France
Plessis, Anne, Paris, France
Thierry, Agnes, Paris, France
PATENT ASSIGNEE(S): Institut Pasteur, Paris, France (non-U.S. corporation)
University Paris-VI, Paris, France (non-U.S. corporation)

	NUMBER	KIND	DATE

PATENT INFORMATION: US 6238924 B1 20010529
APPLICATION INFO.: US 1998-196131 19981120 (9)
RELATED APPLN. INFO.: Continuation of Ser. No. US 1995-417226, filed on 5 Apr 1995, now patented, Pat. No. US 5962327 Division of Ser. No. US 1992-971160, filed on 5 Nov 1992, now patented, Pat. No. US 5474896 Continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Patterson, Jr., Charles L.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 7
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 38 Drawing Figure(s); 24 Drawing Page(s)
LINE COUNT: 1374
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 9 OF 29 USPATFULL
TI Yeast vectors conferring antibiotic resistance
AB A vector having a **gene** for resistance to an antibiotic otherwise capable of killing a host yeast cell, the **gene** being transcribed from a yeast promoter sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:51801 USPATFULL
TITLE: Yeast vectors conferring antibiotic resistance
INVENTOR(S): Yocum, Robert Rogers, Four Orchard La., Lexington, MA, United States 02420

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6214577	B1	20010410
APPLICATION INFO.:	US 1995-466460		19950606 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1990-471673, filed on 24 Jan 1990, now patented, Pat. No. US 5422267, issued on 6 Jun 1995 Continuation of Ser. No. US 1986-864785, filed on 19 May 1986, now abandoned Continuation-in-part of Ser. No. US 1985-736450, filed on 21 May 1985, now abandoned Continuation-in-part of Ser. No. US 1984-612796, filed on 22 May 1984, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Brusca, John S.
LEGAL REPRESENTATIVE: Clark & Elbing LLP
NUMBER OF CLAIMS: 12
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 8 Drawing Figure(s); 7 Drawing Page(s)
LINE COUNT: 757
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 10 OF 29 USPATFULL
TI Plant artificial chromosome compositions and methods
AB The present invention provides for the identification and cloning of functional plant centromeres in Arabidopsis. This will permit construction of stably inherited plant artificial chromosomes (PLACs) which can serve as vectors for the construction of transgenic plant and animal cells. In addition, information on the structure and function of these regions will prove valuable in isolating additional centromeric and centromere related genetic elements and polypeptides from other species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2000:164709 USPATFULL
TITLE: Plant artificial chromosome compositions and methods
INVENTOR(S): Preuss, Daphne, Chicago, IL, United States
Copenhaver, Gregory, Oak Park, IL, United States
PATENT ASSIGNEE(S): University of Chicago, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6156953		20001205
APPLICATION INFO.:	US 1998-90051		19980603 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-48451P	19970603 (60)
	US 1998-73741P	19980205 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Smith, Lynette R.F.
ASSISTANT EXAMINER: Zaghmout, Ousama M-Fail
LEGAL REPRESENTATIVE: Fulbright & Jaworski LLP
NUMBER OF CLAIMS: 27
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 7 Drawing Figure(s); 40 Drawing Page(s)
LINE COUNT: 3342
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 11 OF 29 USPATFULL
TI Genes and proteins controlling cholesterol synthesis
AB The present invention provides isolated nucleic acid sequences which encode a family of HMG-CoA Reductase Degradation (HRD) polypeptides. More particularly, the present invention provides isolated HRD1, HRD2 and HRD3 nucleic acids and the Hrd polypeptides encoded by such nucleic acids, i.e., Hrd1, Hrd2 and Hrd3, respectively. Vectors comprising the nucleic acids are provided. In addition, the present invention provides screening assay related to cholesterol biosynthesis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2000:109966 USPATFULL
TITLE: Genes and proteins controlling cholesterol synthesis
INVENTOR(S): Rine, Jasper D., Moraga, CA, United States
Hampton, Randolph, San Diego, CA, United States
PATENT ASSIGNEE(S): The Regents of the University of California, Berkeley, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6107462		20000822
APPLICATION INFO.:	US 1996-699103		19960816 (8)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-2381P	19950817 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Wax, Robert A.
ASSISTANT EXAMINER: Saidha, Tekchand
LEGAL REPRESENTATIVE: Fish & Richardson P.C.
NUMBER OF CLAIMS: 5
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Figure(s); 10 Drawing Page(s)
LINE COUNT: 3995
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1999:121229 USPATFULL
TITLE:	Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
INVENTOR(S):	Dujon, Bernard, Gif sur Yvette, France Choulika, Andre, Paris, France Colleaux, Laurence, Edinburgh, United Kingdom Fairhead, Cecile, Malakoff, France Perrin, Arnaud, Paris, France Plessis, Anne, Paris, France Thierry, Agnes, Paris, France
PATENT ASSIGNEE(S):	Institut Pasteur Universite Paris-VI, Paris, France (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5962327		19991005
APPLICATION INFO.:	US 1995-417226		19950405 (8)

RELATED APPLN. INFO.:	Division of Ser. No. US 1992-971160, filed on 5 Nov 1992, now patented, Pat. No. US 5474896 which is a continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned
DOCUMENT TYPE:	Utility
FILE SEGMENT:	Granted
PRIMARY EXAMINER:	Patterson, Jr., Charles L.
LEGAL REPRESENTATIVE:	Finnegan, Henderson, Farabow, Garrett, & Dunner, L.L.P.
NUMBER OF CLAIMS:	29
EXEMPLARY CLAIM:	27
NUMBER OF DRAWINGS:	32 Drawing Figure(s); 24 Drawing Page(s)
LINE COUNT:	1874

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1999:106355 USPATFULL
TITLE:	Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
INVENTOR(S):	Dujon, Bernard, Gif sur Yvette, France Choulika, Andre, Paris, France Perrin, Arnaud, Paris, France Nicolas, Jean-Francois, Noisy le Roi, France
PATENT ASSIGNEE(S):	Institut Pasteur, Paris, France (non-U.S. corporation) Universite Peirre et Marie Curie, Paris, France (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5948678		19990907
APPLICATION INFO.:	US 1998-119024		19980720 (9)

RELATED APPLN. INFO.:	Continuation of Ser. No. US 1994-336241, filed on 7 Nov 1994, now patented, Pat. No. US 5792632 which is a

continuation-in-part of Ser. No. US 1992-971160, filed on 5 Nov 1992, now patented, Pat. No. US 5474896 which is a continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Elliott, George C.
ASSISTANT EXAMINER: Schwartzman, Robert
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 14
EXEMPLARY CLAIM: 5
NUMBER OF DRAWINGS: 64 Drawing Figure(s); 46 Drawing Page(s)
LINE COUNT: 2877
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 1999:15718 USPATFULL
TITLE: Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
INVENTOR(S): Dujon, Bernard, Gif Sur Yvette, France
Choulika, Andre, Paris, France
Perrin, Arnaud, Paris, France
Nicolas, Jean-Francois, Noisy Le Roi, France
PATENT ASSIGNEE(S): Institut Pasteur, Paris, France (non-U.S. corporation)
Universite Pierre et Marie Curie, Paris, France (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5866361		19990202
APPLICATION INFO.:	US 1995-465273		19950605 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1994-336241, filed on 7 Nov 1994 which is a continuation-in-part of Ser. No. US 1992-971160, filed on 5 Nov 1992, now patented, Pat. No. US 5474896 which is a continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: LeGuyader, John L.
ASSISTANT EXAMINER: Railey, II, Johnny F.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 8
EXEMPLARY CLAIM: 1,6
NUMBER OF DRAWINGS: 65 Drawing Figure(s); 46 Drawing Page(s)
LINE COUNT: 2752
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 1998:95409 USPATFULL
TITLE: Nucleotide sequence encoding the enzyme I-SceI and the

uses thereof
INVENTOR(S): Dujon, Bernard, Gif Sur Yvette, France
Choulika, Andre, Paris, France
Perrin, Arnaud, Paris, France
Nicolas, Jean-Francois, Noisy Le Roi, France
PATENT ASSIGNEE(S): Institut Pasteur, Paris, France (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5792632		19980811
APPLICATION INFO.:	US 1994-336241		19941107 (8)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1992-971160, filed on 5 Nov 1992, now patented, Pat. No. US 5474896 which is a continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Fleisher, Mindy
ASSISTANT EXAMINER: Weiss, Bonnie D.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 64 Drawing Figure(s); 44 Drawing Page(s)
LINE COUNT: 2804
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 16 OF 29 USPATFULL
TI Biosynthesis of zeaxanthin and glycosylated zeaxanthin in genetically engineered hosts
AB DNA segments encoding the Erwinia herbicola enzymes geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase, DNA variants and analogs thereof encoding an enzyme exhibiting substantially the same biological activity, vectors containing those DNA segments, host cells containing the vectors and methods for producing those enzymes, zeaxanthin and zeaxanthin diglucoside by recombinant DNA technology in transformed host organisms are disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 97:101985 USPATFULL
TITLE: Biosynthesis of zeaxanthin and glycosylated zeaxanthin in genetically engineered hosts
INVENTOR(S): Ausich, Rodney L., Glen Ellyn, IL, United States
Brinkhaus, Friedhelm Luetke, Lisle, IL, United States
Mukharji, Indrani, Evanston, IL, United States
Proffitt, John H., Oak Park, IL, United States
Yarger, James G., St. Charles, IL, United States
Yen, Huei-Che Bill, Naperville, IL, United States
PATENT ASSIGNEE(S): Amoco Corporation, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5684238		19971104
APPLICATION INFO.:	US 1993-96623		19930722 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1991-805061, filed on 9 Dec 1991, now abandoned which is a continuation-in-part of Ser. No. US 1991-662921, filed on 28 Feb 1991, now abandoned which is a continuation-in-part of Ser. No. US 1990-562674, filed on 3 Aug 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-525551, filed on 18 May 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-487613,

filed on 2 Mar 1990, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Chereskin, Che S.
LEGAL REPRESENTATIVE: Welsh & Katz, Ltd.
NUMBER OF CLAIMS: 57
EXEMPLARY CLAIM: 4,9
NUMBER OF DRAWINGS: 45 Drawing Figure(s); 45 Drawing Page(s)
LINE COUNT: 6275
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 29 USPATFULL
TI Beta-carotene biosynthesis in genetically engineered hosts
AB DNA segments encoding the Erwinia herbicola enzymes geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H and lycopene cyclase, vectors containing those DNA segments, host cells containing the vectors and methods for producing those enzymes and beta-carotene by recombinant DNA technology in transformed host organisms are disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 97:70914 USPATFULL
TITLE: Beta-carotene biosynthesis in genetically engineered hosts
INVENTOR(S): Ausich, Rodney L., Glen Ellyn, IL, United States
Brinkhaus, Friedhelm Luetke, Lisle, IL, United States
Mukharji, Indrani, Evanston, IL, United States
Proffitt, John, Oak Park, IL, United States
Yarger, James, St. Charles, IL, United States
Yen, Huei-Che Bill, Naperville, IL, United States
PATENT ASSIGNEE(S): Amoco Corporation, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5656472		19970812
APPLICATION INFO.:	US 1995-473512		19950607 (8)

RELATED APPLN. INFO.: Division of Ser. No. US 1993-95726, filed on 21 Jul 1993, now patented, Pat. No. US 5530188 which is a continuation-in-part of Ser. No. US 1991-662921, filed on 28 Feb 1991, now abandoned which is a continuation-in-part of Ser. No. US 1990-562674, filed on 3 Aug 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-525551, filed on 18 May 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-487613, filed on 2 Mar 1990, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Wax, Robert A.
ASSISTANT EXAMINER: Saidha, Tekchand
LEGAL REPRESENTATIVE: Welsh & Katz, Ltd.
NUMBER OF CLAIMS: 15
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 33 Drawing Figure(s); 33 Drawing Page(s)
LINE COUNT: 4950
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 29 USPATFULL
TI Manufacturing of xylitol using recombinant microbial hosts
AB Novel methods for the synthesis of xylitol are described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 97:42780 USPATFULL

TITLE: Manufacturing of xylitol using recombinant microbial hosts
INVENTOR(S): Harkki, Anu M., Espoo, Finland
Myasnikov, Andrey N., Kantvik, Finland
Apajalahti, Juha H. A., Helsinki, Finland
Pastinen, Ossi A., Kantvik, Finland
PATENT ASSIGNEE(S): Xyrofin Oy, Kotka, Finland (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5631150		19970520
APPLICATION INFO.:	US 1995-368395		19950103 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1993-110672, filed on 24 Aug 1993, now abandoned which is a continuation-in-part of Ser. No. US 1992-973325, filed on 5 Nov 1992, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Elliott, George C.
LEGAL REPRESENTATIVE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
NUMBER OF CLAIMS: 29
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Figure(s); 13 Drawing Page(s)
LINE COUNT: 2158
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 29 USPATFULL
TI Lycopene biosynthesis in genetically engineered hosts
AB DNA segments encoding the Erwinia enzymes geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase and phytoene dehydrogenase-4H, vectors containing those DNA segments, host cells containing the vectors and methods for producing those enzymes and lycopene by recombinant DNA technology in transformed host organisms are disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 96:55943 USPATFULL
TITLE: Lycopene biosynthesis in genetically engineered hosts
INVENTOR(S): Ausich, Rodney L., Glen Ellyn, IL, United States
Brinkhaus, Friedhelm L., Lisle, IL, United States
Mukharji, Indrani, Evanston, IL, United States
Proffitt, John, Oak Park, IL, United States
Yarger, James, St. Charles, IL, United States
Yen, Huei-Che B., Naperville, IL, United States
PATENT ASSIGNEE(S): Amoco Corporation, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5530189		19960625
APPLICATION INFO.:	US 1993-96043		19930722 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1991-785568, filed on 30 Oct 1991, now abandoned which is a continuation-in-part of Ser. No. US 1991-662921, filed on 28 Feb 1991, now abandoned which is a continuation-in-part of Ser. No. US 1990-562674, filed on 3 Aug 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-525551, filed on 18 May 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-487613, filed on 2 Mar 1990, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Chereskin, Che S.
LEGAL REPRESENTATIVE: Sroka, Frank J.
NUMBER OF CLAIMS: 6

EXEMPLARY CLAIM: 1,4
NUMBER OF DRAWINGS: 30 Drawing Figure(s); 30 Drawing Page(s)
LINE COUNT: 4229
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 29 USPATFULL
TI Beta-carotene biosynthesis in genetically engineered hosts
AB DNA segments encoding the Erwinia herbicola enzymes geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H and lycopene cyclase, vectors containing those DNA segments, host cells containing the vectors and methods for producing those enzymes and beta-carotene by recombinant DNA technology in transformed host organisms are disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 96:55942 USPATFULL
TITLE: Beta-carotene biosynthesis in genetically engineered hosts
INVENTOR(S): Ausich, Rodney L., Glen Ellyn, IL, United States
Brinkhaus, Friedhelm L., Lisle, IL, United States
Mukharji, Indrani, Evanston, IL, United States
Proffitt, John, Oak Park, IL, United States
Yarger, James, St. Charles, IL, United States
Yen, Huei-Che B., Naperville, IL, United States
PATENT ASSIGNEE(S): Amoco Corporation, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5530188		19960625
APPLICATION INFO.:	US 1993-95726		19930721 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1991-785566, filed on 30 Oct 1991, now abandoned which is a continuation-in-part of Ser. No. US 1991-662921, filed on 28 Feb 1991, now abandoned which is a continuation-in-part of Ser. No. US 1990-562674, filed on 3 Aug 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-525551, filed on 18 May 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-487613, filed on 2 Mar 1990, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Chereskin, Che S.
LEGAL REPRESENTATIVE: Sroka, Frank J.
NUMBER OF CLAIMS: 7
EXEMPLARY CLAIM: 4
NUMBER OF DRAWINGS: 33 Drawing Figure(s); 33 Drawing Page(s)
LINE COUNT: 4921
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 29 USPATFULL
TI Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
AB An isolated DNA encoding the enzyme I-SceI is provided. The DNA sequence can be incorporated in cloning and expression vectors, transformed cell lines and transgenic animals. The vectors are useful in **gene** mapping and site-directed insertion of genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 95:110345 USPATFULL
TITLE: Nucleotide sequence encoding the enzyme I-SceI and the uses thereof
INVENTOR(S): Dujon, Bernard, Gif sur Yvette, France
Choulika, Andre, Paris, France
Colleaux, Laurence, Edinburgh, Scotland

Fairhead, Cecile, Malakoff, France
Perrin, Arnaud, Paris, France
Plessis, Anne, Paris, France
Thierry, Agnes, Paris, France

PATENT ASSIGNEE(S): Institut Pasteur, both of, France (non-U.S. corporation)
Universite Paris-VI, both of, France (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5474896		19951212
APPLICATION INFO.:	US 1992-971160		19921105 (7)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1992-879689, filed on 5 May 1992, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Parr, Margaret
ASSISTANT EXAMINER: Campbell, Eggerton
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner
NUMBER OF CLAIMS: 2
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 38 Drawing Figure(s); 22 Drawing Page(s)
LINE COUNT: 1641
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 29 USPATFULL
TI Industrial yeast comprising an integrated glucoamylase **gene**
AB A vector having a **gene** for resistance to an antibiotic otherwise capable of killing a host yeast cell, the **gene** being transcribed from a yeast promoter sequence and the vector being capable of being integrated into a chromosome of the host yeast cell; and a diploid or greater ploidy yeast cell transformed by such a vector with heterologous DNA.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 95:50091 USPATFULL
TITLE: Industrial yeast comprising an integrated glucoamylase **gene**
INVENTOR(S): Yocum, Robert R., 180 Jason St., Arlington, MA, United States 02174
Daves, Robert S., Reading, MA, United States
Chen, Michael C., Lexington, MA, United States
PATENT ASSIGNEE(S): Yocum, Robert R., Lexington, MA, United States (U.S. individual)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5422267		19950606
APPLICATION INFO.:	US 1990-471673		19900124 (7)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1986-864785, filed on 19 May 1986, now abandoned which is a continuation-in-part of Ser. No. US 1985-736450, filed on 21 May 1985, now abandoned And a continuation-in-part of Ser. No. US 1985-736565, filed on 21 May 1985, now abandoned which is a continuation-in-part of Ser. No. US 1984-612796, filed on 22 May 1984, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Schwartz, Richard A.
ASSISTANT EXAMINER: Carter, Philip W.
LEGAL REPRESENTATIVE: Fish & Richardson
NUMBER OF CLAIMS: 56
EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 13 Drawing Figure(s); 7 Drawing Page(s)
LINE COUNT: 1092
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 23 OF 29 USPATFULL
TI Process for transformation of yarrowia lipolytica
AB Process for transformation of Yarrowia lipolytica, vectors useful therefor comprising DNA of a microbial vector and chromosomal DNA of Y. lipolytica and transformants comprising said vectors in E. coli and Y. lipolytica, and integrative shuttle vectors for Escherichia-Yarrowia transgeneric cloning. Said vectors or subclones thereof enable creation of Y. lipolytica cloning vectors into which specific or random segments of DNA can be inserted and the resulting vectors used to transform a suitable host microbe, especialy Y. lipolytica, to improve the fermentation characteristics thereof and hence their industrial utilization.

The methodology described permits the cloning of genes from a **gene** library of Y. lipolytica by complementation with an integrating vector.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 91:100279 USPATFULL
TITLE: Process for transformation of yarrowia lipolytica
INVENTOR(S): Davidow, Lance S., Groton, CT, United States
DeZeeuw, John R., Groton, CT, United States
PATENT ASSIGNEE(S): Pfizer Inc., New York, NY, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5071764		19911210
APPLICATION INFO.:	US 1989-400201		19890829 (7)

DISCLAIMER DATE: 20061114
RELATED APPLN. INFO.: Continuation of Ser. No. US 1984-634505, filed on 25 Jul 1984, now patented, Pat. No. US 4880741
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Teskin, Robin L.
LEGAL REPRESENTATIVE: Richardson, Peter C., Lumb, J. Trevor, Benson, Gregg C.
NUMBER OF CLAIMS: 20
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 6 Drawing Figure(s); 6 Drawing Page(s)
LINE COUNT: 1286
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 24 OF 29 USPATFULL
TI Trains of yeast for the expression of heterologous genes
AB The GAL4 protein is rate-limiting in quantity as a positive regulator for galactose-inducible promoters in strains of yeast. Novel strains are described in which the GAL4 protein can be overproduced in a regulatable fashion. These strains are useful for the regulatable expression in yeast of heterologous genes whose expression is driven by a galactose-inducible promoter.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 91:96289 USPATFULL
TITLE: Trains of yeast for the expression of heterologous genes
INVENTOR(S): Hopper, James E., Lebanon, PA, United States
Schultz, Loren D., Harleysville, PA, United States
Hofmann, Kathryn J., King of Prussia, PA, United States
Ellis, Ronald W., Overbrook Hills, PA, United States
PATENT ASSIGNEE(S): Merck & Co., Inc., NJ, United States (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 5068185		19911126	
APPLICATION INFO.:	US 1986-884114		19860710	(6)

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Schwartz, Richard A.
ASSISTANT EXAMINER: Ellis, J.
LEGAL REPRESENTATIVE: Perrella, Donald J., Pfeiffer, Hesna J., Levitt, Julian S.
NUMBER OF CLAIMS: 12
EXEMPLARY CLAIM: 7
NUMBER OF DRAWINGS: 7 Drawing Figure(s); 8 Drawing Page(s)
LINE COUNT: 533
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 25 OF 29 USPATFULL
TI Construction of new .alpha.-galactosidase producing yeast strains and the industrial application of these strains
AB The objects of this invention are new Saccharomyces cerevisiae yeast strains into which .alpha.-galactosidase **gene** (MEL.sup.+) has been transferred by using recombinant DNA methods. Baker's and distiller's yeasts producing .alpha.-galactosidase, are utilizable in the corresponding industry, because they are able to utilize the raffinose present in molasses, which results in greater yield of yeast (or ethanol) and reduction or elimination of the costs associated with biological oxygen demand (B.O.D.) in the effluent from factories. The improved ability of brewer's yeasts to produce .alpha.-galactosidase provides a sensitive method for monitoring pasteurization of beer.

The new yeast strains prepared by using recombinant DNA methods produce more .alpha.-galactosidase than naturally occurring .alpha.-galactosidase producing yeast strains.

Also methods for marking yeast strains and for producing stable transformants of yeasts are presented.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 91:82149 USPATFULL
TITLE: Construction of new .alpha.-galactosidase producing yeast strains and the industrial application of these strains
INVENTOR(S): Liljestrom, Pirkko L., Vantaa, Finland
Tubb, Roy S., Deal, England
Korhola, Matti P., Helsinki, Finland
PATENT ASSIGNEE(S): Alko Ltd., Helsinki, Finland (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 5055401		19911008	
APPLICATION INFO.:	US 1987-36649		19870410	(7)

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Teskin, Robin L.
LEGAL REPRESENTATIVE: Sterne, Kessler, Goldstein & Fox
NUMBER OF CLAIMS: 33
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Figure(s); 10 Drawing Page(s)
LINE COUNT: 837
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 26 OF 29 USPATFULL
TI Process for transformation of Yarrowia lipolytica

AB Process for transformation of Yarrowia lipolytica, vectors useful therefor comprising DNA of a microbial vector and chromosomal DNA of Y. lipolytica and transformants comprising said vectors in E. coli and Y. lipolytica, and integrative shuttle vectors for Escherichia-Yarrowia transgeneric cloning. Said vectors or subclones thereof enable creation of Y. lipolytica cloning vectors into which specific or random segments of DNA can be inserted and the resulting vectors used to transform a suitable host microbe, especially Y. lipolytica, to improve the fermentation characteristics thereof and hence their industrial utilization.

The methodology described permits the cloning of genes from a **gene** library of Y. lipolytica by complementation with an integrating vector.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	89:92447 USPATFULL
TITLE:	Process for transformation of Yarrowia lipolytica
INVENTOR(S):	Davidow, Lance S., Groton, CT, United States DeZeeuw, John R., Stonington, CT, United States
PATENT ASSIGNEE(S):	Pfizer Inc., New York, NY, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 4880741		19891114
APPLICATION INFO.:	US 1984-634505		19840725 (6)

RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 1983-539591, filed on 6 Oct 1983, now abandoned
DOCUMENT TYPE:	Utility
FILE SEGMENT:	Granted
PRIMARY EXAMINER:	Huleatt, Jayme A.
LEGAL REPRESENTATIVE:	Richardson, Peter C., Lumb, J. Trevor, Benson, Gregg C.
NUMBER OF CLAIMS:	87
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	8 Drawing Figure(s); 7 Drawing Page(s)
LINE COUNT:	1476

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 27 OF 29 USPATFULL

TI Novel host strain for transformation of Yarrowia lipolytica

AB A Yarrowia lipolytia strain (PC-30827) ATCC 20688 which is utilized as a suitable host for cloning. The strain is a double auxotroph and requires medium supplemented with leucine and uracil for growth.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	86:69730 USPATFULL
TITLE:	Novel host strain for transformation of Yarrowia lipolytica
INVENTOR(S):	DeZeeuw, John R., Stonington, CT, United States
PATENT ASSIGNEE(S):	Pfizer Inc., New York, NY, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 4628033		19861209
APPLICATION INFO.:	US 1983-539363		19831006 (6)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	Granted
PRIMARY EXAMINER:	Wiseman, Thomas G.
ASSISTANT EXAMINER:	Huleatt, Jayme A.
LEGAL REPRESENTATIVE:	Knuth, Charles J., Frost, Albert E., Richardson, Peter C.
NUMBER OF CLAIMS:	3

EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Figure(s); 4 Drawing Page(s)
LINE COUNT: 853
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 28 OF 29 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
TI Multiple tandem integrations of transforming DNA sequences in **yeast chromosome** suggest a mechanism for **integrative transformation** by homologous recobination.
AB In yeast, the fate of linear DNA molecules upon transformation is determined by the existence of sequence homology between chromosomes and the ends of the transforming molecule. To understand the mechanism of integration of transforming DNA, we have studied the influence of DNA concentration on the frequency and type of transformants obtained, using either non-replicative or replicative plasmids. In both cases, increasing DNA concentration results in multiple tandem repeats integrated into the chromosome containing the homologous target sequence. When a diploid strain is transformed, multiple tandem repeats occur in only one of the two homologous chromosomes at a time. The frequency distribution of the different types of integrants observed indicates non-independent integration events likely to result from plasmid-plasmid interaction prior to chromosome integration. In addition, our results define the proper conditions for optimized **gene** targetting or **gene** rescue experiments.
ACCESSION NUMBER: 93353123 EMBASE
DOCUMENT NUMBER: 1993353123
TITLE: Multiple tandem integrations of transforming DNA sequences in **yeast chromosome** suggest a mechanism for **integrative transformation** by homologous recobination.
AUTHOR: Plessis A.; Dujon B.
CORPORATE SOURCE: Unite de Genet. Molec. des Levures, Institut Pasteur, 25 Rue du Docteur Roux,F-75724 Paris Cedex, France
SOURCE: Gene, (1993) 134/1 (41-50).
ISSN: 0378-1119 CODEN: GENED6
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

L5 ANSWER 29 OF 29 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
TI Isolation and characterization of the RNA2+, RNA4+, and RNA11+ genes of saccharomyces cerevisiae.
AB We used genetic complementation to isolate DNA fragments that encode the Saccharomyces cerevisiae genes RNA2+, RNA4+, and RNA11+ and to localize the genes on the cloned DNA fragments. RNA blot-hydridization analyses coupled with genetic analyses indicated that RNA2+ is coded by a 3.0-kilobase (kb) transcript, RNA4+ is coded by a 1.6-kb transcript, and RNA11+ is coded by a 1.3-kb or a 1.7-kb transcript or both; none of the cloned genes contains detectable introns. All three genes were transcribed into messages of very low abundance (.apprx.20 times lower than a ribosomal protein message). DNA blot-hybridization revealed that all cloned genes are represented only once in the **yeast chromosome**. mRNA for RNA2+ and RNA4+ is produced in approximate proportion to **gene** dosage, whereas RNA11+ transcription appears to be not nearly so dependent on **gene** dosage. On a medium-copy plasmid (5 to 10 copies per cell), each cloned **gene** complemented mutations only in its own **gene**, indicating that each **gene** encodes in unique function. Genetic analysis by **integrative transformation** indicated that we cloned the RNA2+, RNA4+, and RNA11+ structural genes and not second-site suppressors.
ACCESSION NUMBER: 85022705 EMBASE

DOCUMENT NUMBER: 1985022705
TITLE: Isolation and characterization of the RNA2+, RNA4+, and RNA11+ genes of saccharomyces cerevisiae.
AUTHOR: Soltyk A.; Tropak M.; Friesen J.D.
CORPORATE SOURCE: Department of Medical Genetics, University of Toronto, Toronto, Ont. M5S 1A8, Canada
SOURCE: Journal of Bacteriology, (1984) 160/3 (1093-1100). CODEN: JOBAAY
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 004 Microbiology
LANGUAGE: English

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NEWS 20	Aug 19	IFIPAT, IFICDB, and IFIUDB have been reloaded
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NEWS 22	Aug 26	Sequence searching in REGISTRY enhanced
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NEWS 25	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 26	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 27	Oct 21	EVENTLINE has been reloaded
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NEWS 29	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 30	Oct 25	MEDLINE SDI run of October 8, 2002
NEWS 31	Nov 18	DKILIT has been renamed APOLLIT
NEWS 32	Nov 25	More calculated properties added to REGISTRY
NEWS 33	Dec 02	TIBKAT will be removed from STN
NEWS 34	Dec 04	CSA files on STN
NEWS 35	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 36	Dec 17	TOXCENTER enhanced with additional content
NEWS 37	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS 38	Dec 30	ISMEC no longer available
NEWS 39	Jan 13	Indexing added to some pre-1967 records in CA/CAPLUS
NEWS 40	Jan 21	NUTRACEUT offering one free connect hour in February 2003
NEWS 41	Jan 21	PHARMAML offering one free connect hour in February 2003
NEWS 42	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS 43	Feb 13	CANCERLIT is no longer being updated
NEWS 44	Feb 24	METADEX enhancements
NEWS 45	Feb 24	PCTGEN now available on STN

NEWS 46 Feb 24 TEMA now available on STN
NEWS 47 Feb 26 NTIS now allows simultaneous left and right truncation
NEWS 48 Feb 26 PCTFULL now contains images
NEWS 49 Mar 04 SDI PACKAGE for monthly delivery of multifile SDI results

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=> s yeast replication origin
L1 106 YEAST REPLICATION ORIGIN

=> s l1 and 2 micrometer replicon
L2 0 L1 AND 2 MICROMETER REPLICON

=> s l1 and two micrometer replicon
L3 0 L1 AND TWO MICROMETER REPLICON

=> s exogenous gene
L4 1579 EXOGENOUS GENE

=> s autonomous replicating sequence
L5 93 AUTONOMOUS REPLICATING SEQUENCE

=> s l5 and l1
L6 4 L5 AND L1

=> d l6 ti abs ibib tot

L6 ANSWER 1 OF 4 USPATFULL
TI New yeast-bacteria shuttle vector
AB The functional analysis of genes frequently requires the manipulation of large genomic regions. A yeast-bacteria shuttle vector is described,

that can be used to clone large regions of DNA by homologous recombination. The important feature of present invention is the presence of the a bacterial replication origin, which allows large DNA insert capacity. The utility of this vector lies in its ability to isolate, manipulate and maintain large fragments in bacteria and yeast, allowing for mutagenesis by yeast genetics and simplified preparation of plasmid DNA in bacteria.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:243162 USPATFULL
TITLE:	New yeast-bacteria shuttle vector
INVENTOR(S):	Bradshaw, M. Suzanne, Cincinnati, OH, UNITED STATES Bollekens, Jacques A., Brussels, BELGIUM Ruddle, Frank H., New Haven, CT, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002132348	A1	20020919
APPLICATION INFO.:	US 2000-729043	A1	20001204 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1998-95372, filed on 10 Jun 1998, GRANTED, Pat. No. US 6221588 Continuation of Ser. No. US 1996-761704, filed on 6 Dec 1996, GRANTED, Pat. No. US 5866404

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-8250P	19951206 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	Morgan & Finnegan LLP, 345 Park Avenue, New York, NY, 10154
NUMBER OF CLAIMS:	13
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	5 Drawing Page(s)
LINE COUNT:	806

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 2 OF 4 USPATFULL

TI Yeast-bacteria shuttle vector

AB The functional analysis of genes frequently requires the manipulation of large genomic regions. A yeast-bacteria shuttle vector is described, that can be used to clone large regions of DNA by homologous recombination. The important feature of present invention is the presence of the a bacterial replication origin, which allows large DNA insert capacity. The utility of this vector lies in its ability to isolate, manipulate and maintain large fragments in bacteria and yeast, allowing for mutagenesis by yeast genetics and simplified preparation of plasmid DNA in bacteria.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1999:15760 USPATFULL
TITLE:	Yeast-bacteria shuttle vector
INVENTOR(S):	Bradshaw, M. Suzanne, Cincinnati, OH, United States Bollekens, Jacques A., Brussels, Belgium Ruddle, Frank H., New Haven, CT, United States
PATENT ASSIGNEE(S):	Yale University, New Haven, CT, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5866404		19990202
APPLICATION INFO.:	US 1996-761704		19961206 (8)

	NUMBER	DATE

PRIORITY INFORMATION:	US 1995-8250P	19951206 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	Granted	
PRIMARY EXAMINER:	Railey, II, Johnny F.	
LEGAL REPRESENTATIVE:	Morgan & Finnegan, L.L.P.	
NUMBER OF CLAIMS:	13	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	8 Drawing Figure(s); 5 Drawing Page(s)	
LINE COUNT:	850	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 3 OF 4 USPATFULL

TI Expression of recombinant hemoglobin and hemoglobin variants in yeast

AB The invention is directed to a substantially pure mammalian globin chain or heme-binding fragment thereof. The invention is further directed to recombinant DNA vectors capable of expressing at least one globin chain or substantially homologous variant thereof in yeast. The invention also relates to methods for expressing at least one globin chain or substantially homologous variant thereof in yeast. Expressed alpha-like globin and beta-like globin chains or variants thereof may be combined with a source of heme to produce hemoglobin or a substantially homologous variant thereof. Additionally, expressed gamma-globin chains may be combined with a source of heme to produce hemoglobin or a substantially homologous variant thereof. The invention also relates to methods for expressing hemoglobin or variants thereof in yeast where the heme is produced by the yeast and ligated to globins to form hemoglobin in vivo. The hemoglobin produced by the methods of the present invention may be used in applications requiring a physiological oxygen carrier such as in blood substitute solutions and as in plasma expanders or in applications requiring a physiological oxygen carrier.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1998:131569 USPATFULL
TITLE:	Expression of recombinant hemoglobin and hemoglobin variants in yeast
INVENTOR(S):	De Angelo, Joseph, Hamtramck, MI, United States Motwani, Nalini M., Troy, MI, United States Bajwa, Wajeeh, Canton, MI, United States Bonaventura, Joseph, Beaufort, NC, United States
PATENT ASSIGNEE(S):	Apex Bioscience, Inc., Durham, NC, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5827693		19981027
APPLICATION INFO.:	US 1995-484686		19950607 (8)
RELATED APPLN. INFO.:	Continuation of Ser. No. US 1994-368407, filed on 29 Dec 1994, now abandoned which is a continuation of Ser. No. US 1992-876290, filed on 29 Apr 1992, now abandoned which is a continuation-in-part of Ser. No. US 1991-684611, filed on 12 Apr 1991, now abandoned which is a continuation-in-part of Ser. No. US 1990-614359, filed on 14 Nov 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-509918, filed on 16 Apr 1990, now abandoned		
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	Granted		
PRIMARY EXAMINER:	Carlson, Karen		
LEGAL REPRESENTATIVE:	Pennie & Edmonds LLP		
NUMBER OF CLAIMS:	185		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	79 Drawing Figure(s); 69 Drawing Page(s)		
LINE COUNT:	6892		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 4 OF 4 USPATFULL
TI Yeast expression vectors
AB There are described a number of plasmid vectors suitable for the expression of genetic material, at various levels in yeasts. The plasmids each comprise a yeast selective marker, a **yeast replication origin** and a yeast promoter positioned relative to a unique restriction site in such a way that expression may be obtained of a polypeptide coding sequence inserted at the restriction site. The promoters used are derived from the 5' region of a gene coding for a yeast glycolytic enzyme e.g. phosphoglycerate kinase (PGK), or from the 5' region of the yeast TRP1 gene. In one Example a plasmid contains a promoter derived from both the 3' and 5' regions of the PGK gene. The replication systems used involve the yeast 2.mu. replication origin or an **autonomous replicating sequence** (ARS) stabilized with an ARS stabilizing sequence (ASS). The replication systems allow for a choice of high or low copy number per cell. The promoter sequences allow for a choice of high or low expression level. A kit including vectors having a combination of these alternative features is described. Yeast expression vectors including a gene for coding for human interferon-.alpha. are described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 86:56487 USPATFULL
TITLE: Yeast expression vectors
INVENTOR(S): Kingsman, Alan J., Islip, England
Kingsman, Susan M., Islip, England
PATENT ASSIGNEE(S): Celltech Limited, Berkshire, England (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 4615974		19861007	
APPLICATION INFO.:	US 1982-408826		19820817	(6)

	NUMBER	DATE
PRIORITY INFORMATION:	GB 1981-25934	19810825
	GB 1982-8422	19820323
	GB 1982-17496	19820616

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Tanenholtz, Alvin E.
LEGAL REPRESENTATIVE: Cushman, Darby & Cushman
NUMBER OF CLAIMS: 11
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 19 Drawing Figure(s); 19 Drawing Page(s)
LINE COUNT: 719
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l1 ti abs ibib 1-10

L1 ANSWER 1 OF 106 MEDLINE
TI Interaction of fission yeast ORC with essential adenine/thymine stretches in replication origins.
AB BACKGROUND: Eukaryotic DNA replication is initiated from distinct regions on the chromosome. However, the mechanism for recognition of replication origins is not known for most eukaryotes. In fission yeast, replication origins are isolated as autonomously replicating sequences (ARSs). Multiple adenine/thymine clusters are essential for replication, but no short consensus sequences are found. In this paper, we examined the interaction of adenine/thymine clusters with the replication initiation

factor ORC. RESULTS: The SpOrc1 or SpOrc2 immunoprecipitates (IPs) containing at least four subunits of SpORC, interacted with the ars2004 fragment, which is derived from a predominant replication origin on the chromosome. SpORC-IPs preferentially interacted with two regions of the ars2004, which consist of consecutive adenines and AAAAT repeats and are essential for ARS activity. The nucleotide sequences required for the interaction with SpORC-IPs correspond closely to those necessary for in vivo ARS activity. CONCLUSION: Our results suggest that the SpORC interacts with adenine/thymine stretches, which have been shown to be the most important component in the fission **yeast replication origin**. The presence of multiple SpORC-binding sites, with certain sequence variations, is characteristic for the fission yeast replication origins.

ACCESSION NUMBER: 2001610278 MEDLINE
DOCUMENT NUMBER: 21541274 PubMed ID: 11683912
TITLE: Interaction of fission yeast ORC with essential adenine/thymine stretches in replication origins.
AUTHOR: Takahashi T; Masukata H
CORPORATE SOURCE: Department of Biology, Graduate School of Science, Osaka University, 1-1 Machikaneyama-cho, Toyonaka, Osaka 560-0043 Japan.
SOURCE: GENES TO CELLS, (2001 Oct) 6 (10) 837-49. Journal code: 9607379. ISSN: 1356-9597.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011102
Last Updated on STN: 20020301
Entered Medline: 20020228

L1 ANSWER 2 OF 106 MEDLINE
TI Structure-function relationships in replication origins of the yeast Saccharomyces cerevisiae: higher-order structural organization of DNA in regions flanking the ARS consensus sequence.
AB In order to better understand the involvement of the DNA molecule in the replication initiation process we have characterized the structure of the DNA at Autonomously Replicating Sequences (ARSs) in Saccharomyces cerevisiae. Using a new method for anti-bent DNA analysis, which allowed us to take into account the bending contribution of each successive base plate, we have investigated the higher-order structural organization of the DNA in the region which immediately surrounds the ARS consensus sequence (ACS). We have identified left- and right-handed anti-bent DNAs which flank this consensus sequence. The data show that this organization correlates with an active ACS. Analysis of the minimum nucleotide sequence providing ARS function to plasmids reveals an example where the critical nucleotides are restricted to the ACS and the right-handed anti-bent DNA domain, although most of the origins considered contained both left- and right-handed anti-bent DNAs. Moreover, mutational analysis shows that the right-handed form is necessary in order to sustain a specific DNA conformation which is correlated with the level of plasmid maintenance. A model for the role of these individual structural components of the **yeast replication origin** is presented. We discuss the possible role of the right-handed anti-bent DNA domain, in conjunction with the ACS, in the process of replication initiation, and potentialities offered by the combination of left- and right-handed structural components in origin function.

ACCESSION NUMBER: 2000388479 MEDLINE
DOCUMENT NUMBER: 20361288 PubMed ID: 10905353
TITLE: Structure-function relationships in replication origins of the yeast Saccharomyces cerevisiae: higher-order structural organization of DNA in regions flanking the ARS consensus sequence.

AUTHOR: Marilley M
CORPORATE SOURCE: Regulation Genique et Fonctionnelle et microscopie Champ Proche RGFCP, UPRES 2059, IFR CNRS 57, Universite de la Mediterranee, Faculte de Medecine, Marseille, France.. Monique.Marilley@medecine.univ-mrs.fr
SOURCE: MOLECULAR AND GENERAL GENETICS, (2000 Jun) 263 (5) 854-66. Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000818
Last Updated on STN: 20000818
Entered Medline: 20000808

L1 ANSWER 3 OF 106 MEDLINE
TI Clustered adenine/thymine stretches are essential for function of a fission **yeast replication origin**.
AB We have determined functional elements required for autonomous replication of the Schizosaccharomyces pombe ars2004 that acts as an intrinsic chromosomal replication origin. Internal deletion analysis of a 940-bp fragment (ars2004M) showed three regions, I to III, to be required for autonomously replicating sequence (ARS) activity. Eight-base-pair substitutions in the 40-bp region I, composed of arrays of adenines on a DNA strand, resulted in a great reduction of ARS activity. Substitutions of region I with synthetic sequences showed that no specific sequence but rather repeats of three or more consecutive adenines or thymines, without interruption by guanine or cytosine, are required for the ARS activity. The 65-bp region III contains 11 repeats of the AAAAT sequence, while the 165-bp region II has short adenine or thymine stretches and a guanine- and cytosine-rich region which enhances ARS activity. All three regions in ars2004M can be replaced with 40-bp poly(dA/dT) fragments without reduction of ARS activity. Although spacer regions in the ars2004M enhance ARS activity, all could be deleted when an 40-bp poly(dA/dT) fragment was added in place of region I. Our results suggest that the origin activity of fission yeast replicators depends on the number of adenine/thymine stretches, the extent of their clustering, and presence of certain replication-enhancing elements.
ACCESSION NUMBER: 1999421954 MEDLINE
DOCUMENT NUMBER: 99421954 PubMed ID: 10490609
TITLE: Clustered adenine/thymine stretches are essential for function of a fission **yeast replication origin**.
AUTHOR: Okuno Y; Satoh H; Sekiguchi M; Masukata H
CORPORATE SOURCE: Department of Biology, Graduate School of Science, Osaka University, Toyonaka, Japan.
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (1999 Oct) 19 (10) 6699-709. Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000209
Last Updated on STN: 20000209
Entered Medline: 20000203

L1 ANSWER 4 OF 106 MEDLINE
TI Multiple orientation-dependent, synergistically interacting, similar domains in the ribosomal DNA replication origin of the fission yeast, Schizosaccharomyces pombe.
AB Previous investigations have shown that the fission yeast,

Schizosaccharomyces pombe, has DNA replication origins (500 to 1500 bp) that are larger than those in the budding yeast, Saccharomyces cerevisiae (100 to 150 bp). Deletion and linker substitution analyses of two fission yeast origins revealed that they contain multiple important regions with AT-rich asymmetric (abundant A residues in one strand and T residues in the complementary strand) sequence motifs. In this work we present the characterization of a third fission **yeast replication origin**, ars3001, which is relatively small (approximately 570 bp) and responsible for replication of ribosomal DNA. Like previously studied fission yeast origins, ars3001 contains multiple important regions. The three most important of these regions resemble each other in several ways: each region is essential for origin function and is at least partially orientation dependent, each region contains similar clusters of A+T-rich asymmetric sequences, and the regions can partially substitute for each other. These observations suggest that ars3001 function requires synergistic interactions between domains binding similar proteins. It is likely that this requirement extends to other fission yeast origins, explaining why such origins are larger than those of budding yeast.

ACCESSION NUMBER: 1999038234 MEDLINE
DOCUMENT NUMBER: 99038234 PubMed ID: 9819416
TITLE: Multiple orientation-dependent, synergistically interacting, similar domains in the ribosomal DNA replication origin of the fission yeast, Schizosaccharomyces pombe.
AUTHOR: Kim S M; Huberman J A
CORPORATE SOURCE: Department of Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.
CONTRACT NUMBER: GM49294 (NIGMS)
P30 CA16056 (NCI)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (1998 Dec) 18 (12) 7294-303.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981224

L1 ANSWER 5 OF 106 MEDLINE
TI Activation of a **yeast replication origin** near a double-stranded DNA break.
AB Irradiation in the G1 phase of the cell cycle delays the onset of DNA synthesis and transiently inhibits the activation of replication origins in mammalian cells. It has been suggested that this inhibition is the result of the loss of torsional tension in the DNA after it has been damaged. Because irradiation causes DNA damage at an undefined number of nonspecific sites in the genome, it is not known how cells respond to limited DNA damage, and how replication origins in the immediate vicinity of a damage site would behave. Using the sequence-specific HO endonuclease, we have created a defined double-stranded DNA break in a centromeric plasmid in G1-arrested cells of the yeast Saccharomyces cerevisiae. We show that replication does initiate at the origin on the cut plasmid, and that the plasmid replicates early in the S phase after linearization in vivo. These observations suggest that relaxation of a supercoiled DNA domain in yeast need not inactivate replication origins within that domain. Furthermore, these observations rule out the possibility that the late replication context associated with chromosomal termini is a consequence of DNA ends.

ACCESSION NUMBER: 95011561 MEDLINE
DOCUMENT NUMBER: 95011561 PubMed ID: 7926750
TITLE: Activation of a **yeast replication**

origin near a double-stranded DNA break.
AUTHOR: Raghuraman M K; Brewer B J; Fangman W L
CORPORATE SOURCE: Department of Genetics SK-50, University of Washington, Seattle 98195.
CONTRACT NUMBER: 18926
SOURCE: GENES AND DEVELOPMENT, (1994 Mar 1) 8 (5) 554-62.
Journal code: 8711660. ISSN: 0890-9369.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199411
ENTRY DATE: Entered STN: 19941222
Last Updated on STN: 19941222
Entered Medline: 19941116

L1 ANSWER 6 OF 106 MEDLINE
TI Loading of a DNA helicase on the DNA unwinding element in the **yeast replication origin**: mechanism of DNA replication in a model system.
AB We found that initiation of DNA replication occurs from the region containing the yeast autonomously replicating sequence 1 (ARS1), by incubating negatively supercoiled plasmid DNA with the proteins required for SV40 DNA replication in addition to DNA gyrase (Ishimi, Y., & Matsumoto, K. (1993) Proc. Natl. Acad. Sci. U.S.A. 90, 5399-5403). Here, the mechanism of DNA replication and the roles of the replication proteins in this model system were analyzed. Both SV40 T antigen as a DNA helicase and multisubunit human single-stranded DNA binding protein (HSSB) (also called RP-A) were required for the initial step of DNA synthesis. Furthermore, it has been shown that T antigen plays an essential role in the initiation of DNA replication from the ARS region in this system. The digestion of negatively supercoiled DNA with the single-strand-specific nuclease P1 revealed that regions containing A, B, and C domains of ARS1 can be unwound under the conditions used for DNA replication. Footprinting with KMnO4 indicated that T antigen interacted with the unwound B domain where initiation of DNA replication mainly occurred. When circular DNAs of different negative-superhelical densities were replicated in the absence of DNA gyrase, short fragments were synthesized from the ARS region in proportion to its density and they were elongated by addition of HeLa topoisomerase I, which inhibits the initiation of DNA replication in this system. (ABSTRACT TRUNCATED AT 250 WORDS)
ACCESSION NUMBER: 94162294 MEDLINE
DOCUMENT NUMBER: 94162294 PubMed ID: 8117739
TITLE: Loading of a DNA helicase on the DNA unwinding element in the **yeast replication origin**: mechanism of DNA replication in a model system.
AUTHOR: Ishimi Y; Matsumoto K
CORPORATE SOURCE: Mitsubishi Kasei Institute of Life Sciences, Tokyo, Japan.
SOURCE: BIOCHEMISTRY, (1994 Mar 8) 33 (9) 2733-40.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199404
ENTRY DATE: Entered STN: 19940412
Last Updated on STN: 19940412
Entered Medline: 19940407

L1 ANSWER 7 OF 106 MEDLINE
TI Protein-DNA interactions at a **yeast replication origin**.
AB An understanding of the protein-DNA interactions in vivo at origins of DNA replication in eukaryotes is essential to delineate the mechanism of

initiation of DNA synthesis and its control in the cell cycle. In the yeast Saccharomyces cerevisiae, a family of sequences known as autonomously replicating sequences (ARSs) function as origins of bidirectional DNA replication on plasmids and, in several instances, also in their normal chromosomal location. Here we use nucleotide resolution genomic footprinting to investigate the association of proteins with ARS1. Nuclease protection patterns indicate that at least two different cellular factors interact with functional elements in ARS1. The first seems to be ARS-binding factor 1. The second seems to be a novel protein that generates extensive protection over the essential ARS consensus sequence and phased DNaseI-sensitive sites across a functionally important flanking sequence. Hypersensitivity of this region to cleavage by copper phenanthroline indicates that it is under torsional strain, analogous to that produced at transcriptional start sites by assembly of an initiation complex. The protection in situ is similar to that generated by the origin recognition complex (ORC) protein.

ACCESSION NUMBER: 92252913 MEDLINE
DOCUMENT NUMBER: 92252913 PubMed ID: 1579168
TITLE: Protein-DNA interactions at a **yeast replication origin**.
AUTHOR: Diffley J F; Cocker J H
CORPORATE SOURCE: Imperial Cancer Research Fund, Potters Bar, Hertfordshire, UK.
SOURCE: NATURE, (1992 May 14) 357 (6374) 169-72.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920619
Last Updated on STN: 19970203
Entered Medline: 19920611

L1 ANSWER 8 OF 106 MEDLINE
TI DNA helical stability accounts for mutational defects in a **yeast replication origin**.
AB Earlier studies on the H4 autonomously replicating sequence (ARS) identified a DNA unwinding element (DUE), a required sequence that is hypersensitive to single-strand-specific nucleases and serves to facilitate origin unwinding. Here we demonstrate that a DUE can be identified in the C2G1 ARS, a chromosomal replication origin, by using a computer program that calculates DNA helical stability from the base sequence. The helical stability minima correctly predict the location and hierarchy of the nuclease-hypersensitive sites in a C2G1 ARS plasmid. Nucleotide-level mapping shows that the nuclease-hypersensitive site at the ARS spans a 100-base-pair sequence in the required 3'-flanking region. Mutations that stabilize the DNA helix in the broad 3'-flanking region reduce or abolish ARS-mediated plasmid replication, indicating that helical instability is required for origin function. The level of helical instability is quantitatively related to the replication efficiency of the ARS mutants. Multiple copies of either a consensus-related sequence present in the C2G1 ARS or the consensus sequence itself in synthetic ARS elements contribute to DNA helical instability. Our findings indicate that a DUE is a conserved component of the C2G1 ARS and is a major determinant of replication origin activity.

ACCESSION NUMBER: 92212887 MEDLINE
DOCUMENT NUMBER: 92212887 PubMed ID: 1557369
TITLE: DNA helical stability accounts for mutational defects in a **yeast replication origin**.
AUTHOR: Natale D A; Schubert A E; Kowalski D
CORPORATE SOURCE: Molecular and Cellular Biology Department, Roswell Park Cancer Institute, Buffalo, NY 14263.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE

UNITED STATES OF AMERICA, (1992 Apr 1) 89 (7) 2654-8.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199205
ENTRY DATE: Entered STN: 19920515
Last Updated on STN: 19920515
Entered Medline: 19920506

L1 ANSWER 9 OF 106 MEDLINE
TI The DNA unwinding element in a **yeast replication origin** functions independently of easily unwound sequences present elsewhere on a plasmid.
AB We have previously identified a DNA unwinding element (DUE) in autonomously replicating sequences (ARSs) and demonstrated a correlation between single-strand-specific nuclease hypersensitivity of the DUE and ARS-mediated plasmid replication in yeast. The DUE in the H4 ARS is the most easily unwound sequence in a supercoiled DNA molecule, in the context of the Ylp5 plasmid. To determine whether sequences which are more readily unwound than the ARS can influence replication activity, we have inserted such sequences, called 'torsional sinks', into the plasmids at a site distal to the ARS. We show that the torsional sink sequences effect reduction or elimination of the nuclease hypersensitivity of a variety of H4 ARS derivatives. However, we detect no difference in the in vivo replication activity of an individual ARS plasmid with or without a torsional sink. Thus, the function of the DUE in a **yeast replication origin** is unaffected by easily unwound sequences present elsewhere on the same plasmid.
ACCESSION NUMBER: 91067445 MEDLINE
DOCUMENT NUMBER: 91067445 PubMed ID: 2174542
TITLE: The DNA unwinding element in a **yeast replication origin** functions independently of easily unwound sequences present elsewhere on a plasmid.
AUTHOR: Umek R M; Kowalski D
CORPORATE SOURCE: Department of Molecular and Cellular Biology, Roswell Park Cancer Institute, Buffalo, NY 14263.
CONTRACT NUMBER: GM 30614 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (1990 Nov 25) 18 (22) 6601-5.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199101
ENTRY DATE: Entered STN: 19910308
Last Updated on STN: 19910308
Entered Medline: 19910115

L1 ANSWER 10 OF 106 MEDLINE
TI Thermal energy suppresses mutational defects in DNA unwinding at a **yeast replication origin**.
AB Yeast replication origins contain a DNA sequence element whose biological activity correlates with hypersensitivity to single-strand-specific nucleases in negatively supercoiled plasmids. By using two-dimensional gel electrophoresis of plasmid topoisomers, we demonstrate that thermodynamically stable origin unwinding accounts for the nuclease hypersensitivity and, furthermore, that increased thermal energy facilitates stable origin unwinding in vitro. In living cells, increased thermal energy can suppress origin mutations that raise the free-energy cost for unwinding the nuclease-hypersensitive element. Specifically, mutational defects in autonomously replicating sequence (ARS)-mediated

plasmid replication are less severe in cells grown at 30 degrees C as compared to 23 degrees C. Our findings indicate that the energetics of DNA unwinding at the nuclease-hypersensitive element are biologically important. We call the nuclease-hypersensitive sequence the DNA unwinding element (DUE) and propose that it serves as the entry site for yeast replication enzymes into the DNA helix.

ACCESSION NUMBER: 90207220 MEDLINE
DOCUMENT NUMBER: 90207220 PubMed ID: 2181439
TITLE: Thermal energy suppresses mutational defects in DNA unwinding at a **yeast replication origin**.
AUTHOR: Umek R M; Kowalski D
CORPORATE SOURCE: Department of Molecular and Cellular Biology, Roswell Park Cancer Institute, Buffalo, NY 14263.
CONTRACT NUMBER: GM30614 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1990 Apr) 87 (7) 2486-90. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199005
ENTRY DATE: Entered STN: 19900601
Last Updated on STN: 19900601
Entered Medline: 19900504

=> d his

(FILE 'HOME' ENTERED AT 11:57:07 ON 12 MAR 2003)

FILE 'MEDLINE, USPATFULL' ENTERED AT 12:01:29 ON 12 MAR 2003
L1 106 S YEAST REPLICATION ORIGIN
L2 0 S L1 AND 2 MICROMETER REPLICON
L3 0 S L1 AND TWO MICROMETER REPLICON
L4 1579 S EXOGENOUS GENE
L5 93 S AUTONOMOUS REPLICATING SEQUENCE
L6 4 S L5 AND L1

=> d l5 ti abs ibib 1-10

L5 ANSWER 1 OF 93 MEDLINE
TI Multiple functional elements comprise a Mammalian chromosomal replicator.
AB The structure of replication origins in metazoans is only nominally similar to that in model organisms, such as Saccharomyces cerevisiae. By contrast to the compact origins of budding yeast, in metazoans multiple elements act as replication start sites or control replication efficiency. We first reported that replication forks diverge from an origin 5' to the human c-myc gene and that a 2.4-kb core fragment of the origin displays **autonomous replicating sequence** activity in plasmids and replicator activity at an ectopic chromosomal site. Here we have used clonal HeLa cell lines containing mutated c-myc origin constructs integrated at the same chromosomal location to identify elements important for DNA replication. Replication activity was measured before or after integration of the wild-type or mutated origins using PCR-based nascent DNA abundance assays. We find that deletions of several segments of the c-myc origin, including the DNA unwinding element and transcription factor binding sites, substantially reduced replicator activity, whereas deletion of the c-myc promoter P(1) had only a modest effect. Substitution mutagenesis indicated that the sequence of the DNA unwinding element, rather than the spacing of flanking sequences, is critical. These results identify multiple functional elements essential for c-myc replicator activity.

ACCESSION NUMBER: 2003078377 IN-PROCESS
DOCUMENT NUMBER: 22477406 PubMed ID: 12589000
TITLE: Multiple functional elements comprise a Mammalian chromosomal replicator.
AUTHOR: Liu Guoqi; Malott Michelle; Leffak Michael
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Wright State University School of Medicine, Dayton, Ohio 45435.
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (2003 Mar) 23 (5) 1832-42. Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20030221
Last Updated on STN: 20030221

L5 ANSWER 2 OF 93 MEDLINE
TI Vectors designed for efficient molecular manipulation in Candida albicans.
AB Functional studies on genes of Candida albicans have been hampered by the fact that few vectors are available for efficient cloning and expression in C. albicans, in contrast to Saccharomyces cerevisiae. Here we report that six vectors were constructed for molecular manipulation in C. albicans. All of them contained the **autonomous replicating sequence** ARS2 and the uracil gene as a selective marker. Introduction of multicloning site (MCS) facilitated directional cloning into various convenient restriction sites is discussed. Distal to the MCS, the additions of sequences encoding yeast-enhanced green fluorescent protein 3 (yEGFP3) and the terminator of chitin synthase 2 (TCHS2) enabled us to express an open reading frame (ORF) with its own promoter as a GFP fusion protein, so that its intracellular localization could be easily determined. A vector of 7.4 kb was also constructed to express a cloned ORF as a GFP fusion protein under the control of an inducible MET3 promoter (PMET3) located proximal to the MCS. Since this vector was relatively large in size for expressing ORFs, two additional vectors of 6.7 kb were constructed by inserting PMET3 and TCHS2 proximal and distal to the MCS of the above vector containing MCS only, respectively. These six vectors made it possible to study C. albicans in greater detail. They can be used in identification of a promoter, intracellular localization of a protein, and in the induction of lethal genes.

ACCESSION NUMBER: 2002454765 MEDLINE
DOCUMENT NUMBER: 22200290 PubMed ID: 12210900
TITLE: Vectors designed for efficient molecular manipulation in Candida albicans.
AUTHOR: Park Nok-Hyun; Choi Wonja
CORPORATE SOURCE: Department of Life Sciences, College of Natural Sciences, Ewha Womans University, Seoul 120-750, South Korea.
SOURCE: YEAST, (2002 Sep 15) 19 (12) 1057-66. Journal code: 8607637. ISSN: 0749-503X.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200211
ENTRY DATE: Entered STN: 20020906
Last Updated on STN: 20021212
Entered Medline: 20021104

L5 ANSWER 3 OF 93 MEDLINE
TI A system for dual protein expression in Pichia pastoris and Escherichia coli.
AB We have constructed a novel Pichia pastoris/Escherichia coli dual expression vector for the production of recombinant proteins in both host

systems. In this vector, an E. coli T7 promoter region, including the ribosome binding site from the phage T7 major capsid protein for efficient translation is placed downstream from the yeast alcohol oxidase promoter (AOX). For detection and purification of the target protein, the vector contains an amino-terminal oligohistidine domain (His6) followed by the hemaglutinine epitope (HA) adjacent to the cloning sites. A P. pastoris **autonomous replicating sequence** (PARS) was integrated enabling simple propagation and recovery of plasmids from yeast and bacteria (1). In the present study, the expression of human proteins in P. pastoris and E. coli was compared using this single expression vector. For this purpose we have subcloned a cDNA expression library deriving from human fetal brain (2) into our dual expression T7 vector and investigated 96 randomly picked clones. After sequencing, 29 clones in the correct reading frame have been identified, their plasmids isolated and shuttled from yeast to bacteria. All proteins were expressed soluble in P. pastoris, whereas in E. coli only 31% could be purified under native conditions. Our data indicates that this dual expression vector allows the economic expression and purification of proteins in different hosts without subcloning.

ACCESSION NUMBER: 2001078729 MEDLINE
DOCUMENT NUMBER: 20541628 PubMed ID: 11087676
TITLE: A system for dual protein expression in Pichia pastoris and Escherichia coli.
AUTHOR: Lueking A; Holz C; Gotthold C; Lehrach H; Cahill D
CORPORATE SOURCE: Max-Planck-Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany.
SOURCE: PROTEIN EXPRESSION AND PURIFICATION, (2000 Dec) 20 (3) 372-8.
Journal code: 9101496. ISSN: 1046-5928.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010111

L5 ANSWER 4 OF 93 MEDLINE
TI Determination of the functional domain of a mouse **autonomous replicating sequence**.
AB We previously isolated from mouse cells an **autonomous replicating sequence** (ARS) ARS65 (Ariga, Itani and Iguchi-Ariga, Mol. Cell. Biol. 7, 1-6, 1987). Here we report the nucleotide sequence of ARS65. The sequence from BgIII to EcoRI sites cloned as ARS was 2658 bp long. There exist three interesting domains: a TA repeat, a myc like box (essential sequence for c-myc ARS), and a T rich region. Cloned DNAs containing various segments of pARS65 were transfected to rat 3Y1 cells together with the hygromycinB resistance expression vector, and hygromycinB resistant clones were isolated. Established cell lines transfected with plasmids carrying either a myc-like box or a T rich region harbored the replicated plasmids, indicating that these two elements are necessary for the ARS function of pARS65.

ACCESSION NUMBER: 97356556 MEDLINE
DOCUMENT NUMBER: 97356556 PubMed ID: 9212992
TITLE: Determination of the functional domain of a mouse **autonomous replicating sequence** .
AUTHOR: Hayashi C; Fujino H; Ogata M; Sato Y; Iguchi-Ariga S M; Ariga H
CORPORATE SOURCE: Faculty of Pharmaceutical Sciences, Hokkaido University, Sapporo, Japan.
SOURCE: BIOLOGICAL AND PHARMACEUTICAL BULLETIN, (1997 Jun) 20 (6)

690-3.
Journal code: 9311984. ISSN: 0918-6158.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X70989
ENTRY MONTH: 199708
ENTRY DATE: Entered STN: 19970902
Last Updated on STN: 19990129
Entered Medline: 19970818

L5 ANSWER 5 OF 93 MEDLINE
TI Identification of an essential core element and stimulatory sequences in a Kluyveromyces lactis ARS element, KARS101.
AB A Kluyveromyces lactis chromosomal sequence of 913 bp is sufficient for replication in Saccharomyces cerevisiae and K. lactis. This fragment contains a 12 bp sequence 5'-ATTTATTGTTTT-3' that is related to the S. cerevisiae ACS (ARS consensus sequence). This dodecamer was removed by site-directed mutagenesis and the effect on K. lactis and S. cerevisiae ARS (**autonomous replicating sequence**) activity was determined. The dodecamer is essential for S. cerevisiae ARS function but only contributes to K. lactis ARS activity; therefore, its role in K. lactis is unlikely to be the same as that of the essential S. cerevisiae ACS. A 103 bp subclone was found to retain ARS activity in both yeasts, but the plasmid was very unstable in S. cerevisiae. Deletion and linker substitution mutagenesis of this fragment was undertaken to define the DNA sequence required for K. lactis ARS function and to test whether the sequence required for ARS activity in K. lactis and S. cerevisiae coincide. We found a 39 bp core region essential for K. lactis ARS function flanked by sequences that contribute to ARS efficiency. The instability of the plasmid in S. cerevisiae made a fine-structure analysis of the S. cerevisiae ARS element impossible. However, the sequences that promote high-frequency transformation in S. cerevisiae overlap the essential core of the K. lactis ARS element but have different end-points.
ACCESSION NUMBER: 96417855 MEDLINE
DOCUMENT NUMBER: 96417855 PubMed ID: 8820646
TITLE: Identification of an essential core element and stimulatory sequences in a Kluyveromyces lactis ARS element, KARS101.
AUTHOR: Fabiani L; Frontali L; Newlon C S
CORPORATE SOURCE: Dipartimento di Biologia Cellulare e dello Sviluppo, Universita 'La Sapienza,' Rome, Italy.
CONTRACT NUMBER: GM 35679 (NIGMS)
SOURCE: MOLECULAR MICROBIOLOGY, (1996 Feb) 19 (4) 756-66.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961216

L5 ANSWER 6 OF 93 MEDLINE
TI Cooperation at a distance between silencers and proto-silencers at the yeast HML locus.
AB Transcriptional repression at the silent yeast mating type loci is achieved through the formation of a particular nucleoprotein complex at specific cis-acting elements called silencers. This complex in turn appears to initiate the spreading of a histone binding protein complex into the surrounding chromatin, which restricts accessibility of the region to the transcription machinery. We have investigated long-range, cooperative effects between silencers by studying the repression of a

reporter gene integrated at the HML locus flanked by various combinations of wild-type and mutated silencer sequences. Two silencers can cooperate over >4000 bp to repress transcription efficiently. More importantly, a single binding site for either the repressor activator protein 1 (Rap1), the **autonomous replicating sequence** (ARS) binding factor 1 (Abf1) or the origin recognition complex (ORC) can enhance the action of a distant silencer without acting as a silencer on its own. Functional cooperativity is demonstrated using a quantitative assay for repression, and varies with the affinity of the binding sites used. Since the repression mechanism is Sir dependent, the Rap1, ORC and/or Abf1 proteins bound to distant DNA elements may interact to create an interface of sufficiently high affinity such that Sir-containing complexes bind, nucleating the silent chromatin state.

ACCESSION NUMBER: 96208505 MEDLINE
DOCUMENT NUMBER: 96208505 PubMed ID: 8641284
TITLE: Cooperation at a distance between silencers and proto-silencers at the yeast HML locus.
AUTHOR: Boscheron C; Maillet L; Marcand S; Tsai-Pflugfelder M; Gasser S M; Gilson E
CORPORATE SOURCE: Ecole Normale Superieure de Lyon, France.
SOURCE: EMBO JOURNAL, (1996 May 1) 15 (9) 2184-95.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199607
ENTRY DATE: Entered STN: 19960726
Last Updated on STN: 20030214
Entered Medline: 19960718

L5 ANSWER 7 OF 93 MEDLINE
TI Cis-acting effects of sequences within 2.4-kb upstream of the human c-myc gene on autonomous plasmid replication in HeLa cells.
AB We have used density shift analysis to monitor the **autonomous replicating sequence** (ARS) activity of plasmids containing various DNA fragments from the 5'-flanking region of the human c-myc gene. The ARS activity of certain of these plasmids implied that structures in the c-myc DNA could be recognized for the initiation of replication in the absence of chromosomal integration. The plasmid pNeo.Myc-2.4 contains 2.4 contains 2.4 kb of c-myc 5'-flanking DNA, and replicated semiconservatively as a circular extrachromosomal element. Deletion derivatives of pNeo.Myc-2.4 containing either of two nonoverlapping regions of c-myc DNA semiconservatively incorporated bromodeoxyuridine into discrete populations of heavy-light supercoiled molecules to roughly the same extent as the chromosomal DNA in the same cultures. Some constructs displayed lower ARS activity, implying that distinct cis-acting sequences in the c-myc 5'-flanking DNA may independently affect DNA replication. The ARS activity of two separate c-myc sequences suggests that replication initiation signals are redundant in the c-myc origin. The smallest c-myc insert that displayed substantial ARS activity was 930 bp long and contained three 10/11 matches to the yeast ARS consensus and several additional features found in eukaryotic replication origins.

ACCESSION NUMBER: 95352201 MEDLINE
DOCUMENT NUMBER: 95352201 PubMed ID: 7626216
TITLE: Cis-acting effects of sequences within 2.4-kb upstream of the human c-myc gene on autonomous plasmid replication in HeLa cells.
AUTHOR: McWhinney C; Waltz S E; Leffak M
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Wright State University, Dayton, OH 45435, USA.
SOURCE: DNA AND CELL BIOLOGY, (1995 Jul) 14 (7) 565-79.
Journal code: 9004522. ISSN: 1044-5498.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199509
ENTRY DATE: Entered STN: 19950921
Last Updated on STN: 19970203
Entered Medline: 19950901

L5 ANSWER 8 OF 93 MEDLINE
TI Kluyveromyces marxianus small DNA fragments contain both autonomous replicative and centromeric elements that also function in Kluyveromyces lactis.
AB Two fragments containing both an **autonomous replicating sequence** (ARS) and a centromere have been isolated and sequenced from the yeast Kluyveromyces marxianus. The ARS and centromeric core sequences are only 500 bp apart, but ARS activity could be separated from the centromeric sequences. Centromeric sequences are organized in a similar way to those of budding yeasts: two well-conserved elements: CDEI (5' TCACGTG 3') and CDEIII (5' TNTTCCGAAAGTWAAA 3'), are separated by a 165 bp AT-rich (+/- 90%) CDEII element whose length is twice that of Saccharomyces cerevisiae CDEII but almost identical to that of K. lactis. The ARS-core consensus sequence (5' TTTATTGTT 3') is also similar to that of K. lactis. Both ARS and centromeric elements function in this strain, albeit inefficiently, but not in S. cerevisiae. A third ARS-containing fragment with a different organization has been isolated and sequenced.
ACCESSION NUMBER: 95242837 MEDLINE
DOCUMENT NUMBER: 95242837 PubMed ID: 7725797
TITLE: Kluyveromyces marxianus small DNA fragments contain both autonomous replicative and centromeric elements that also function in Kluyveromyces lactis.
AUTHOR: Iborra F; Ball M M
CORPORATE SOURCE: Laboratoire de Biologie et Genetique Moleculaire, IGM CNRS URA 1354, Orsay, France.
SOURCE: YEAST, (1994 Dec) 10 (12) 1621-9.
Journal code: 8607637. ISSN: 0749-503X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Z31562; GENBANK-Z31563; GENBANK-Z31564
ENTRY MONTH: 199505
ENTRY DATE: Entered STN: 19950605
Last Updated on STN: 19950605
Entered Medline: 19950525

L5 ANSWER 9 OF 93 MEDLINE
TI High-efficiency transformation of Pichia stipitis based on its URA3 gene and a homologous autonomous replication sequence, ARS2.
AB This paper describes the first high-efficiency transformation system for the xylose-fermenting yeast Pichia stipitis. The system includes integrating and autonomously replicating plasmids based on the gene for orotidine-5'-phosphate decarboxylase (URA3) and an **autonomous replicating sequence** (ARS) element (ARS2) isolated from P. stipitis CBS 6054. Ura- auxotrophs were obtained by selecting for resistance to 5-fluoroorotic acid and were identified as ura3 mutants by transformation with P. stipitis URA3. P. stipitis URA3 was cloned by its homology to Saccharomyces cerevisiae URA3, with which it is 69% identical in the coding region. P. stipitis ARS elements were cloned functionally through plasmid rescue. These sequences confer autonomous replication when cloned into vectors bearing the P. stipitis URA3 gene. P. stipitis ARS2 has features similar to those of the consensus ARS of S. cerevisiae and other ARS elements. Circular plasmids bearing the P. stipitis URA3 gene with various amounts of flanking sequences produced 600 to 8,600 Ura+

transformants per micrograms of DNA by electroporation. Most transformants obtained with circular vectors arose without integration of vector sequences. One vector yielded 5,200 to 12,500 Ura+ transformants per micrograms of DNA after it was linearized at various restriction enzyme sites within the P. stipitis URA3 insert. Transformants arising from linearized vectors produced stable integrants, and integration events were site specific for the genomic ura3 in 20% of the transformants examined. Plasmids bearing the P. stipitis URA3 gene and ARS2 element produced more than 30,000 transformants per micrograms of plasmid DNA. Autonomously replicating plasmids were stable for at least 50 generations in selection medium and were present at an average of 10 copies per nucleus.

ACCESSION NUMBER: 95110115 MEDLINE
DOCUMENT NUMBER: 95110115 PubMed ID: 7811063
TITLE: High-efficiency transformation of Pichia stipitis based on its URA3 gene and a homologous autonomous replication sequence, ARS2.
AUTHOR: Yang V W; Marks J A; Davis B P; Jeffries T W
CORPORATE SOURCE: Forest Products Laboratory, U.S. Department of Agriculture, Madison, Wisconsin 53705.
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (1994 Dec) 60 (12) 4245-54.
Journal code: 7605801. ISSN: 0099-2240.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U08628; GENBANK-U08629
ENTRY MONTH: 199501
ENTRY DATE: Entered STN: 19950215
Last Updated on STN: 19960129
Entered Medline: 19950131

L5 ANSWER 10 OF 93 MEDLINE
TI Protein-DNA interactions in the epsilon-globin gene silencer.
AB The developmental control of expression of the human epsilon-globin gene appears to be mediated, at least in part, by a transcriptional silencer in the DNA 5' to the cap site of this gene. We have used site-directed mutagenesis and DNA-protein binding assays to define the active motifs of this epsilon-globin silencer. DNase I foot-printing of the silencer region with K562 cell nuclear extracts defined a sequence, which we designate as the epsilon-globin silencer motif or epsilon GSM (epsilon -278 to -258 base pairs (bp)) containing a region (epsilon -270 to -258) with 90% homology to the yeast mating type silencer, ABF-1 (**autonomous replicating sequence** binding factor one) and which also overlaps at (epsilon -269 to -262) with the human YY1 consensus sequence, an element which mediates transcription repression and activation of viral, mouse, and human genes. The DNase I footprint extended 5' in the silencer region to include an inverted repeat of a six-nucleotide motif (epsilon -267 to -278 bp) which shares 5 of 6 bases with the GATA-1 consensus sequence. In gel mobility shift assays, two specific proteins (A and B) in nuclear extracts from erythroleukemia K562 cells bound to the DNase I-footprinted region. Protein B, associated with epsilon-globin silencer activity in vitro, required an intact epsilon GSM sequence for binding. Mutation of 5 bases within the epsilon GSM in an epsilon-globin promoter-containing fragment extending upstream to 1400 bp in transient transfection assays increased activity by 3.0-fold compared with the native sequence, suggesting that the silencer activity was mediated by the epsilon GSM sequence. We found that protein A could be displaced by a competitor containing the GATA-1 consensus sequence, suggesting that protein A is a GATA-like protein. The region from -267 to -271 within the epsilon GSM and GATA-1 homology region was important for binding of both proteins A and B. These data suggest that protein binding to the epsilon GSM and GATA motifs mediate the negative effect of the silencer on transcription, possibly via direct competition for binding to this DNA

region. Recombinant yeast ABF-1 and human YY1 bound to the epsilon GSM. Mutating three bases (epsilon -259, -262, -264) in the epsilon GSM decreased the binding affinity of protein B and recombinant human YY1 but increased the binding affinity of recombinant yeast ABF-1. Furthermore, competitor containing the YY1 consensus sequence competed for protein B binding, whereas competitor containing a perfect yeast ABF-1 consensus sequence did not.(ABSTRACT TRUNCATED AT 400 WORDS)

ACCESSION NUMBER: 93155191 MEDLINE
DOCUMENT NUMBER: 93155191 PubMed ID: 8429019
TITLE: Protein-DNA interactions in the epsilon-globin gene silencer.
AUTHOR: Peters B; Merezhinskaya N; Diffley J F; Noguchi C T
CORPORATE SOURCE: Laboratory of Chemical Biology, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, Maryland 20892.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1993 Feb 15) 268 (5) 3430-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199303
ENTRY DATE: Entered STN: 19930326
Last Updated on STN: 19970203
Entered Medline: 19930309

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(FILE 'HOME' ENTERED AT 11:57:07 ON 12 MAR 2003)

FILE 'MEDLINE, USPATFULL' ENTERED AT 12:01:29 ON 12 MAR 2003
L1 106 S YEAST REPLICATION ORIGIN
L2 0 S L1 AND 2 MICROMETER REPLICON
L3 0 S L1 AND TWO MICROMETER REPLICON
L4 1579 S EXOGENOUS GENE
L5 93 S AUTONOMOUS REPLICATING SEQUENCE
L6 4 S L5 AND L1

=> s l1 and l4
L7 12 L1 AND L4

=> d l7 ti abs ibib tot

L7 ANSWER 1 OF 12 USPATFULL
TI Novel PN9826 nucleic acids and use thereof
AB Novel PN9826 protein and nucleic acids encoding PN9826 are provided. PN9826-containing protein complexes formed by PN9826 and a PN9826-interacting protein (e.g., LTBP1) are also provided. LTBP1 and PN9826 may be involved in common biological processes such as angiogenesis, metastasis, and cell growth and adhesion. Thus, the protein complexes as well as PN9826 can be used in screening assays to select modulators of PN9826 and the protein complexes formed by PN9826 and LTBP1. The identified modulators can be useful in modulating the functions and activities of PN9826 and protein complexes containing PN9826.

ACCESSION NUMBER: 2003:51206 USPATFULL
TITLE: Novel PN9826 nucleic acids and use thereof
INVENTOR(S): Wettstein, Daniel Albert, Salt Lake City, UT, UNITED STATES
Mauck, Kimberly A., Sandy, UT, UNITED STATES
PATENT ASSIGNEE(S): Myriad Genetics, Incorporated, Salt Lake City, UT,

UNITED STATES, 84108 (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003036163	A1	20030220	
APPLICATION INFO.:	US 2002-195142	A1	20020710	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-304323P	20010710	(60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 30
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Page(s)
LINE COUNT: 5944

L7 ANSWER 2 OF 12 USPATFULL
TI APOA2-interacting proteins and use thereof
AB Protein complexes are provided comprising APOA2 and one or more APOA2-interacting proteins. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with APOA2 and its interacting partners. In addition, methods of detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:30383 USPATFULL
TITLE: APOA2-interacting proteins and use thereof
INVENTOR(S): Bartel, Paul, Salt Lake City, UT, UNITED STATES
Sugiyama, Janice, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S): Myriad Genetics, Incorporated, Salt Lake City, UT (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003022330	A1	20030130	
APPLICATION INFO.:	US 2002-125639	A1	20020418	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-285324P	20010419	(60)
	US 2002-349843P	20020117	(60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
LINE COUNT: 4780
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 12 USPATFULL
TI APOA1-interacting proteins and use thereof
AB Protein complexes are provided comprising APOA1 and one or more APOA1-interacting proteins. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with APOA1 and its interacting partners. In addition, methods of detecting the protein complexes and modulating the

functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:10678 USPATFULL
TITLE:	APOA1-interacting proteins and use thereof
INVENTOR(S):	Bartel, Paul, Salt Lake City, UT, UNITED STATES Szankasi, Philippe, Salt Lake City, UT, UNITED STATES Sugiyama, Janice, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S):	Myriad Genetics, Incorporated, Salt Lake City, UT (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003008373	A1	20030109	
APPLICATION INFO.:	US 2002-124767	A1	20020417	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-284220P	20010417	(60)
	US 2002-354899P	20020206	(60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS:	38
EXEMPLARY CLAIM:	1
LINE COUNT:	4667

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 12 USPATFULL

TI Caspase-7-interacting protein and use thereof

AB Protein complexes are provided comprising Caspase-7 and a Caspase-7-interacting protein. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with Caspase-7 and the Caspase-7-interacting protein. In addition, methods for detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:10629 USPATFULL
TITLE:	Caspase-7-interacting protein and use thereof
INVENTOR(S):	Bartel, Paul, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S):	Myriad Genetics, Incorporated, Salt Lake City, UT (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003008324	A1	20030109	
APPLICATION INFO.:	US 2002-124550	A1	20020417	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-284404P	20010417	(60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS:	38
EXEMPLARY CLAIM:	1
LINE COUNT:	4771

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 12 USPATFULL
TI Mating-based method for detecting protein-protein interaction
AB The present invention provides a mating-based yeast two-hybrid system for determining whether a test polypeptide interacts with another test polypeptide in the presence or absence of one or more test compounds. The system is useful in detecting protein-protein interactions and in identifying compounds capable of modulating protein-protein interactions.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:3404 USPATFULL			
TITLE:	Mating-based method for detecting protein-protein interaction			
INVENTOR(S):	Ostanin, Kirill, Salt Lake City, UT, UNITED STATES			
PATENT ASSIGNEE(S):	Myriad Genetics, Incorporated, Salt Lake City, UT, UNITED STATES (U.S. corporation)			
	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003003439	A1	20030102	
APPLICATION INFO.:	US 2002-186386	A1	20020628	(10)
	NUMBER		DATE	
PRIORITY INFORMATION:	US 2001-302535P		20010629	(60)
DOCUMENT TYPE:	Utility			
FILE SEGMENT:	APPLICATION			
LEGAL REPRESENTATIVE:	MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108			
NUMBER OF CLAIMS:	58			
EXEMPLARY CLAIM:	1			
NUMBER OF DRAWINGS:	18 Drawing Page(s)			
LINE COUNT:	2614			

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 12 USPATFULL
TI FLT4-interacting proteins and use thereof
AB Protein complexes are provided comprising FLT4 and one or more FLT4-interacting proteins. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with FLT4 and its interacting partners. In addition, methods of detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:343965 USPATFULL			
TITLE:	FLT4-interacting proteins and use thereof			
INVENTOR(S):	Sugiyama, Janice, Salt Lake City, UT, UNITED STATES			
PATENT ASSIGNEE(S):	Myriad Genetics, Incorporated, Salt Lake City, UT, UNITED STATES (U.S. corporation)			
	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002197691	A1	20021226	
APPLICATION INFO.:	US 2002-135802	A1	20020429	(10)
	NUMBER		DATE	
PRIORITY INFORMATION:	US 2001-287513P		20010430	(60)
DOCUMENT TYPE:	Utility			
FILE SEGMENT:	APPLICATION			

LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
LINE COUNT: 4778
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 7 OF 12 USPATFULL
TI BCL-XL-interacting protein and use thereof
AB Protein complexes are provided comprising BCL-XL and TCTP. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with BCL-XL and TCTP. In addition, methods for detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:315203 USPATFULL
TITLE: BCL-XL-interacting protein and use thereof
INVENTOR(S): Bartel, Paul, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S): Myriad Genetics, Incorporated, Salt Lake City, UT, UNITED STATES, 84108 (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002177692	A1	20021128	
APPLICATION INFO.:	US 2002-122573	A1	20020415	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-284095P	20010416 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
LINE COUNT: 4757
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 8 OF 12 USPATFULL
TI Tsg101-interacting proteins and use thereof
AB Protein complexes are provided comprising Tsg101 and one or more protein interactors of Tsg101. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with Tsg101 and its interacting partner proteins. In addition, methods of detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:314730 USPATFULL
TITLE: Tsg101-interacting proteins and use thereof
INVENTOR(S): Sugiyama, Janice, Salt Lake City, UT, UNITED STATES
Cimbora, Daniel, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S): Myriad Genetics, Incorporated, Salt Lake City, UT, UNITED STATES, 84108 (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002177207	A1	20021128	
APPLICATION INFO.:	US 2002-98979	A1	20020314	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-276259P	20010314 (60)
	US 2001-304101P	20010710 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
LINE COUNT: 7034
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 12 USPATFULL
TI COX 1-interacting proteins and use thereof
AB Protein complexes are provided comprising COX1 and one or more proteins selected from the group consisting of THR S14 and Opa1. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with COX1 and its interacting partner proteins. In addition, methods of detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:314675 USPATFULL
TITLE: COX 1-interacting proteins and use thereof
INVENTOR(S): Wettstein, Daniel Albert, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S): Myriad Genetics, Incorporated, Salt Lake City, UT (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002177152	A1	20021128	
APPLICATION INFO.:	US 2002-100503	A1	20020318	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-277013P	20010319 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
LINE COUNT: 4721
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 10 OF 12 USPATFULL
TI Survivin-interacting proteins and use thereof
AB Protein complexes are provided comprising survivin and one or more proteins selected from the group consisting of HDLC1, beta-actin, DNA helicase II, COPP, OSTP, SLC8A1, A2-CAT. The protein complexes are useful in screening assays for identifying compounds effective in modulating the protein complexes and in treating and/or preventing diseases and disorders associated with survivin and its interacting partner proteins. In addition, methods of detecting the protein complexes and modulating the functions and activities of the protein complexes or interacting members thereof are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:307902 USPATFULL

TITLE: Survivin-interacting proteins and use thereof
INVENTOR(S): Wettstein, Daniel Albert, Salt Lake City, UT, UNITED STATES
Cimbora, Daniel, Salt Lake City, UT, UNITED STATES
PATENT ASSIGNEE(S): Myriad Genetics, Incorporated, Salt Lake City, UT (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002173026	A1	20021121
APPLICATION INFO.:	US 2002-99924	A1	20020314 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-276179P	20010315 (60)
	US 2001-307233P	20010723 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MYRIAD GENETICS INC., LEGAL DEPARTMENT, 320 WAKARA WAY, SALT LAKE CITY, UT, 84108
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
LINE COUNT: 5137
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 12 USPATFULL
TI Expression of exogenous polypeptides and polypeptide products including hepatitis B surface antigen in yeast cells
AB Novel yeast cell transformation vectors are manufactured and employed in securing expression of exogenous polypeptides in yeast cells. Vectors include promoter/regulator DNA sequences of yeast glyceraldehyde-3-phosphate dehydrogenase gene origins. In an illustrative preferred embodiment, novel immunologically active hepatitis B surface antigen (HBsAg) preparations are isolated from yeast cells transformed with plasmid A.T.C.C. 40053. These HBsAg preparations of yeast origin may be incorporated into vaccine compositions useful in developing immunological responses protective against infection by hepatitis B virus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 93:24824 USPATFULL
TITLE: Expression of exogenous polypeptides and polypeptide products including hepatitis B surface antigen in yeast cells
INVENTOR(S): Bitter, Grant A., Thousand Oaks, CA, United States
PATENT ASSIGNEE(S): Amgen Inc., Thousand Oaks, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5198348		19930330
APPLICATION INFO.:	US 1990-586819		19900924 (7)

DISCLAIMER DATE: 20071211
RELATED APPLN. INFO.: Continuation of Ser. No. US 1988-231599, filed on 8 Aug 1988, now patented, Pat. No. US 4977092 which is a continuation of Ser. No. US 1985-748712, filed on 26 Jun 1985, now abandoned which is a continuation of Ser. No. US 1982-412707, filed on 30 Aug 1982, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Martinell, James
LEGAL REPRESENTATIVE: Marshall, O'Toole, Gerstein, Murray & Bicknell
NUMBER OF CLAIMS: 1
EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 4 Drawing Figure(s); 3 Drawing Page(s)
LINE COUNT: 872
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 12 USPATFULL
TI Expression of exogenous polypeptides and polypeptide products including hepatitis B surface antigen in yeast cells
AB Novel yeast cell transformation vectors are manufactured and employed in securing expression of exogenous polypeptides in yeast cells. Vectors include promoter/regulator DNA sequences of yeast glyceraldehyde-3-phosphate dehydrogenase gene origins. In an illustrative preferred embodiment, novel immunologically active hepatitis B surface antigen (HBsAg) preparations are isolated from yeast cells transformed with plasmid A.T.C.C. 40053. These HBsAg preparations of yeast origin may be incorporated into vaccine compositions useful in developing immunological responses protective against infection by hepatitis B virus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 90:95025 USPATFULL
TITLE: Expression of exogenous polypeptides and polypeptide products including hepatitis B surface antigen in yeast cells
INVENTOR(S): Bitter, Grant A., Thousand Oaks, CA, United States
PATENT ASSIGNEE(S): Amgen, Thousand Oaks, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 4977092		19901211
APPLICATION INFO.:	US 1988-231599		19880808 (7)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1985-748712, filed on 26 Jun 1985, now abandoned which is a continuation of Ser. No. US 1982-412707, filed on 30 Aug 1982, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Martinell, James
LEGAL REPRESENTATIVE: Marshall, O'Toole, Gerstein, Murray & Bicknell
NUMBER OF CLAIMS: 10
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 975
CAS INDEXING IS AVAILABLE FOR THIS PATENT.